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OM protein - protein search, using sw model

Run on: October 5, 2005, 11:14:40 ; Search time 24 Seconds  
(without alignments)  
2376.329 Million cell updates/sec

Title: US-09-445-614B-2  
Perfect score: 4004  
Sequence: 1 MTSPPSSPVRLTLDGGQE.....EDEDGASENYYVPVQLQSN 764

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4004	100.0	764	3	US-09-235-451-36
2	4004	100.0	764	4	US-09-978-303-36
3	3988.5	99.6	889	4	US-09-132-316-2
4	3051.5	76.2	761	3	US-09-235-451-4
5	3036.5	75.8	727	3	US-09-978-303-4
6	3036.5	75.8	727	3	US-09-235-451-23
7	3036.5	75.8	727	3	US-09-978-303-23
8	1689	42.2	843	3	US-09-235-451-25
9	1689	42.2	843	4	US-09-978-303-25
10	1652	41.3	838	3	US-09-235-451-2
11	1652	41.3	838	4	US-09-132-316-3
12	1652	41.3	838	4	US-09-667-422-9
13	1652	41.3	838	4	US-09-978-303-2
14	1651.5	41.2	839	4	US-09-667-422-4
15	1645.5	41.1	839	3	US-09-197-636-2
16	1644.5	41.1	839	3	US-09-197-636-8
17	1644.5	41.1	839	3	US-09-235-451-34
18	1644.5	41.1	839	4	US-09-978-303-34
19	1639.5	40.9	839	4	US-09-533-220A-2
20	1639.5	40.9	839	4	US-09-949-016-6937
21	1638.5	40.9	839	3	US-09-197-636-4
22	1486	37.1	798	4	US-09-949-016-9926
23	1471	36.7	871	4	US-09-500-123-7
24	1440	36.0	279	4	US-09-149-476-500
25	1298.5	32.4	742	4	US-09-500-123-12
26	1281	32.0	811	4	US-09-500-123-9
27	969	24.2	511	4	US-09-667-422-5

28	634	15.8	725	4	US-09-350-457A-2	Sequence 2, Appli
29	607.5	15.2	727	4	US-09-350-457A-4	Sequence 4, Appli
30	430.5	10.8	511	4	US-09-759-143-909	Sequence 909, App
31	274	6.8	57	3	US-09-235-451-15	Sequence 15, Appl
32	274	6.8	57	4	US-09-978-303-15	Sequence 15, Appl
33	272	6.8	232	4	US-09-149-476-623	Sequence 623, App
34	247	6.2	71	3	US-09-235-451-14	Sequence 14, Appl
35	247	6.2	71	4	US-09-978-303-14	Sequence 6, Appli
36	225	5.6	1709	4	US-09-949-016-9882	Sequence 9882, Ap
37	223.5	5.6	978	4	US-09-949-016-11563	Sequence 11563, A
38	215	5.4	974	4	US-09-392-812A-4	Sequence 4, Appli
39	212.5	5.3	1619	4	US-09-392-812A-2	Sequence 2, Appli
40	190.5	4.8	1704	4	US-09-759-143-910	Sequence 910, App
41	179	4.5	134	4	US-09-949-016-6340	Sequence 6340, Ap
42	168.5	4.2	759	4	US-09-172-977-4	Sequence 4, Appli
43	151	3.8	1839	2	US-09-404-108-4	Sequence 4, Appli
44	151	3.8	1839	4	US-09-949-016-7659	Sequence 7659, Ap
45	151	3.8	2753	4	US-09-949-016-7659	Sequence 7659, Ap

ALIGNMENTS

RESULT 1  
US-09-235-451-36  
; Sequence 36, Application US/09235451  
; GENERAL INFORMATION:  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Julius, David J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF  
; FILE OF INVENTION: 9076/084CIP  
; CURRENT APPLICATION NUMBER: US/09/235,451  
; CURRENT FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/072,151  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 08/915,461  
; PRIOR FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 36  
; LENGTH: 764  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; ORGANISM: US-09-235-451-36

Query Match 100.0%; Score 4004; DB 3; Length 764;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSPPSSPVRLTLDGGQSGSEARGKLDGSGGLPPMESQFGEDRKFAPIRVNLNY 60  
Db 1 MTSPPSSPVRLTLDGGQSGSEARGKLDGSGGLPPMESQFGEDRKFAPIRVNLNY 60

Qy 61 RKTGTASQDPNPFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTEGSTGTCL 120  
Db 61 RKTGTASQDPNPFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTEGSTGTCL 120

Qy 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSAHIAIEKRSLOCVK 180  
Db 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSAHIAIEKRSLOCVK 180

Qy 181 LLVENGANVHARACGRFFQKGQTCFYFGEPLSLAACTQWDVSVYLLNPHQPASLOA 240  
Db 181 LLVENGANVHARACGRFFQKGQTCFYFGEPLSLAACTQWDVSVYLLNPHQPASLOA 240

Qy 241 TDSQGNVTALVMI SDNSAENALVTSMYDGLQAGARLCPTVQLEDIRNLQDLTPKL 300  
Db 241 TDSQGNVTALVMI SDNSAENALVTSMYDGLQAGARLCPTVQLEDIRNLQDLTPKL 300

Qy 301 AAKEGKIEIFRHILQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEANSVLEITAF 360

Db 301 AAKEGKIEIFRHILQREFSGLSHLRKPTWCYGPVRVSLYDLASVDSCEENSVLBIIAF 360  
QY 361 HCKSPHRHVMVLEPLNKLLOAKWDLILPKPFFLNFLCNLIYMFIFTAVAYHOPTLKKQAA 420  
Db 361 HCKSPHRHVMVLEPLNKLLOAKWDLILPKPFFLNFLCNLIYMFIFTAVAYHOPTLKKQAA 420  
QY 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQWYFWRRHVFIWISFIDSYSFEILFLFOALL 480  
Db 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQWYFWRRHVFIWISFIDSYSFEILFLFOALL 480  
QY 481 TVVSQVLCFLAEWYLPVLVSALVGLWMLLYYTRGFQHTGIYSVMIQKVILRDLRLFL 540  
Db 481 TVVSQVLCFLAEWYLPVLVSALVGLWMLLYYTRGFQHTGIYSVMIQKVILRDLRLFL 540  
QY 541 IYLVFLFGFAVALVSLSQEAWRPEAFTGPNATESVQPMGQDEGNGAQYRGILEASLEL 600  
Db 541 IYLVFLFGFAVALVSLSQEAWRPEAFTGPNATESVQPMGQDEGNGAQYRGILEASLEL 600  
QY 601 FKPTIGMGLAFQEOQLHFRGMVLLILLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660  
Db 601 FKPTIGMGLAFQEOQLHFRGMVLLILLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660  
QY 661 KLOKALSVLEMENGYWCKKQORAGVMLTVGTPDGSPPDERWCFRVEEVNWNASWEQTLPT 720  
Db 661 KLOKALSVLEMENGYWCKKQORAGVMLTVGTPDGSPPDERWCFRVEEVNWNASWEQTLPT 720  
QY 721 LCEDPSGAGVPRTELENPVLASPPKEDGEGASENYYVPVQLQSN 764  
Db 721 LCEDPSGAGVPRTELENPVLASPPKEDGEGASENYYVPVQLQSN 764

RESULT 2  
US-09-978-303-36  
; Sequence 36, Application US/09978303  
; Patent No. 6790629  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: Nucleic acid sequences encoding  
; TITLE OF INVENTION: capsaisin receptor and capsaisin receptor-related  
; TITLE OF INVENTION: polypeptides and uses thereof  
; FILE REFERENCE: UCAL084CON  
; CURRENT APPLICATION NUMBER: US/09/978,303  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/235,451  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/072,151  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 08/915,461  
; PRIOR FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 764  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-978-303-36

Query Match 100.0%; Score 4004; DB 4; Length 764;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTSPPSSPVFRLETTDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFPAPQIRVNLNY 60  
Db 1 MTSPPSSPVFRLETTDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFPAPQIRVNLNY 60  
QY 61 RKGTSASQDPNRFDRDLRFLNFAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120  
Db 61 RKGTSASQDPNRFDRDLRFLNFAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120  
QY 121 MKAVNLKDGVNACILPLQLQIDRDSGNPQLVNAQCTDDYYRGHSALHIAIEKRSLSQCVK 180

Db 121 MKAVNLKDGVNACILPLQLQIDRDSGNPQLVNAQCTDDYYRGHSALHIAIEKRSLSQCVK 180  
QY 181 LLVENGANVHARACGRFFQKGGCTCFYFGELPLSLAACTKQWDVSYLLENPHQASLOA 240  
Db 181 LLVENGANVHARACGRFFQKGGCTCFYFGELPLSLAACTKQWDVSYLLENPHQASLOA 240  
QY 241 TDSQGNTVLHALVMSDNSAENIALVTSMYDGLLQAGARLCTPVOLEDIRNLQDLTPLKL 300  
Db 241 TDSQGNTVLHALVMSDNSAENIALVTSMYDGLLQAGARLCTPVOLEDIRNLQDLTPLKL 300  
QY 301 AAKEGKIEIFRHILQREFSGLSHLRKPTWCYGPVRVSLYDLASVDSCEENSVLBIIAF 360  
Db 301 AAKEGKIEIFRHILQREFSGLSHLRKPTWCYGPVRVSLYDLASVDSCEENSVLBIIAF 360  
QY 361 HCKSPHRHVMVLEPLNKLLOAKWDLILPKPFFLNFLCNLIYMFIFTAVAYHOPTLKKQAA 420  
Db 361 HCKSPHRHVMVLEPLNKLLOAKWDLILPKPFFLNFLCNLIYMFIFTAVAYHOPTLKKQAA 420  
QY 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQWYFWRRHVFIWISFIDSYSFEILFLFOALL 480  
Db 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQWYFWRRHVFIWISFIDSYSFEILFLFOALL 480  
QY 481 TVVSQVLCFLAEWYLPVLVSALVGLWMLLYYTRGFQHTGIYSVMIQKVILRDLRLFL 540  
Db 481 TVVSQVLCFLAEWYLPVLVSALVGLWMLLYYTRGFQHTGIYSVMIQKVILRDLRLFL 540  
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Db 541 IYLVFLFGFAVALVSLSQEAWRPEAFTGPNATESVQPMGQDEGNGAQYRGILEASLEL 600  
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Db 601 FKPTIGMGLAFQEOQLHFRGMVLLILLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660  
QY 661 KLOKALSVLEMENGYWCKKQORAGVMLTVGTPDGSPPDERWCFRVEEVNWNASWEQTLPT 720  
Db 661 KLOKALSVLEMENGYWCKKQORAGVMLTVGTPDGSPPDERWCFRVEEVNWNASWEQTLPT 720  
QY 721 LCEDPSGAGVPRTELENPVLASPPKEDGEGASENYYVPVQLQSN 764  
Db 721 LCEDPSGAGVPRTELENPVLASPPKEDGEGASENYYVPVQLQSN 764

RESULT 3  
US-09-132-316-2  
; Sequence 2, Application US/09132316B  
; Patent No. 6444440  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul E.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Vanilloid Receptor-2  
; FILE REFERENCE: 1488.1110000  
; CURRENT APPLICATION NUMBER: US/09/132,316B  
; CURRENT FILING DATE: 1998-08-11  
; EARLIER APPLICATION NUMBER: US 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 889  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-132-316-2  
Query Match 99.6%; Score 3988.5; DB 4; Length 889;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 763; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MTSPPSSPVFRLETTDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFPAPQIRVNLNY 60

Db 127 MTSPPSSPVFRLETTLDGGQDGEADRGKLDGSGLPMPMESQFQGEDRKFAFQIRVNLNY 186  
QY  
Db 61 RKGTTGASQDPPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTGSGTKTCL 120  
QY  
Db 187 RKGTTGASQDPPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTGSGTKTCL 246  
QY  
Db 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYVYRGHSAHIAIEKRSIQCVK 180  
QY  
Db 247 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYVYRGHSAHIAIEKRSIQCVK 306  
QY  
Db 181 LLVANGANVHARACGRFFQKGQGTCTFYFGBELPLSLAACTKQWDVSVYLLLENPHQPASLOA 240  
QY  
Db 307 LLVANGANVHARACGRFFQKGQGTCTFYFGBELPLSLAACTKQWDVSVYLLLENPHQPASLOA 366  
QY  
Db 241 TDSQGNVTLHALVMIWISONSANALVTSMYDGLLOAGARLCPPTVQLEDIRNLQDITPLKL 300  
QY  
Db 367 TDSQGNVTLHALVMIWISONSANALVTSMYDGLLOAGARLCPPTVQLEDIRNLQDITPLKL 426  
QY  
Db 301 AAKEGKIEIFRHILQREFSGLSHRKFTWCYGPVRSVLYDLASVDSCEENSVLIEIIAF 360  
QY  
Db 427 AAKEGKIEIFRHILQREFSGLSHRKFTWCYGPVRSVLYDLASVDSCEENSVLIEIIAF 486  
QY  
Db 361 HCKSPHRRMVVLEPLNKLQAKWDLIPKFFLNLNLIYMFIFTAVAYHQPTLKKQAA 420  
QY  
Db 487 HCKSPHRRMVVLEPLNKLQAKWDLIPKFFLNLNLIYMFIFTAVAYHQPTLKK-AA 545  
QY  
Db 421 PHLKAEGVNSMLTGHILILGIGIYLLVGLQWYFWRHVPFIWISFIDSYPFELFLFOALL 480  
QY  
Db 546 PHLKAEGVNSMLTGHILILGIGIYLLVGLQWYFWRHVPFIWISFIDSYPFELFLFOALL 605  
QY  
Db 481 TVVSQVLCFLAIEWLPLVLSALVGLWNLNLIYTRGFQHTGIYSVMIQKVLRLDLRFL 540  
QY  
Db 606 TVVSQVLCFLAIEWLPLVLSALVGLWNLNLIYTRGFQHTGIYSVMIQKVLRLDLRFL 665  
QY  
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Db 666 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEQDEGNGAQYRGILEASLEL 725  
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Db 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYLLNLIYTRGFQHTGIYSVMIQKVLRLDLRFL 660  
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Db 726 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYLLNLIYTRGFQHTGIYSVMIQKVLRLDLRFL 785  
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Db 661 KLOKATSVLEWNGYMWCRKQKQAGVMTVGTGPDGSPDERWCFRVEEVNWSWEOQLTPT 720  
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Db 786 KLOKATSVLEWNGYMWCRKQKQAGVMTVGTGPDGSPDERWCFRVEEVNWSWEOQLTPT 845  
QY  
Db 721 LCEDPGAGVPRITLENVPLASPPKEDGEGASEENYVPVQLQSN 764  
QY  
Db 846 LCEDPGAGVPRITLENVPLASPPKEDGEGASEENYVPVQLQSN 889

RESULT 4  
US-09-235-451-4  
; Sequence 4, Application US/09235451  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: 9076/084CIP  
; CURRENT APPLICATION NUMBER: US/09/235,451  
; CURRENT FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/072,151  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 08/915,461  
; PRIOR FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 761  
; TYPE: PRT

; ORGANISM: R. rattus  
US-09-235-451-4  
Query Match 76.2%; Score 3051.5; DB 3; Length 761;  
Best Local Similarity 77.7%; Pred. No. 1.9e-278; Indels 17; Gaps 7;  
Matches 598; Conservative 62; Mismatches 93;  
QY 1 MTSPPSSPVFRLETTLDGGQDGEADRGKLDGSGLPMPMESQFQGEDRKFAFQIRVNLNY 60  
Db 1 MTSASGPPAFRLTSDGDEEGNAEVNKGQE----PPMPESPQREDNRSSPOIKVNLNF 56  
QY 61 ----RKGTCG--SQPDNPFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTGSGT 115  
Db 57 IKRPKNTSAPSQBQDFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTGSGT 116  
QY 116 GKTCLMKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYVYRGHSAHIAIEKRS 175  
Db 117 GKTCLMKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYVYRGHSAHIAIEKRS 176  
QY 176 LQCVKLLVANGANVHARACGRFFQKGQGTCTFYFGBELPLSLAACTKQWDVSVYLLLENPHQ 235  
Db 177 LQCVKLLVANGANVHARACGRFFQKGQGTCTFYFGBELPLSLAACTKQWDVSVYLLLENPHQ 236  
QY 236 ASLQATDSQNTVTLHALVMIWISONSANALVTSMYDGLLOAGARLCPPTVQLEDIRNLQD 295  
Db 237 ASLEATDSLGNTVTLHALVMIADNSPENSALVIMYDGLLOAGARLCPPTVQLEDIRNLQD 296  
QY 296 TPLKAAKEGKIEIFRHILQREFSG--LSHLRKFTEWCYGPVRSVLYDLASVDSCEENS 354  
Db 297 TPLKAAKEGKIEIFRHILQREFSGYQPLSRKFTWCYGPVRSVLYDLSSVDSWENSV 356  
QY 355 LEIIAFHCKSPHRRMVVLEPLNKLQAKWDLIPKFFLNLNLIYMFIFTAVAYHQPT 414  
Db 357 LEIIAFHCKSPHRRMVVLEPLNKLQAKWDLIPKFFLNLNLIYMFIFTAVAYHQPT 416  
QY 415 LKKQAAPHKAEVNSMLTGHILILGIGIYLLVGLQWYFWRHVPFIWISFIDSYPFEL 474  
Db 417 LQQAIPSSKATFGESMLLGHILILGIGIYLLVGLQWYFWRHVPFIWISFIDSYPFEL 476  
QY 475 LQQAIPSSKATFGESMLLGHILILGIGIYLLVGLQWYFWRHVPFIWISFIDSYPFEL 534  
Db 477 LQQAIPSSKATFGESMLLGHILILGIGIYLLVGLQWYFWRHVPFIWISFIDSYPFEL 536  
QY 535 LRLFLIYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEQDEGNGAQYRGIL 594  
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QY 595 EASLELFKFTIGMELAFQELHFRGMVLLLLAYVLLTYLLNLIYTRGFQHTGIYSVMIQK 654  
Db 595 DASLELFKFTIGMELAFQELHFRGMVLLLLAYVLLTYLLNLIYTRGFQHTGIYSVMIQK 654  
QY 655 DSWSIWKLOKATSVLEWNGYMWCRKQKQAGVMTVGTGPDGSPDERWCFRVEEVNWS 713  
Db 655 NWSIWKLOKATSVLEWNGYMWCRKQKQAGVMTVGTGPDGSPDERWCFRVEEVNWS 714  
QY 714 WEOTLPTLCEDPGAGVPRITLENVPLASPPKEDGEGASEENYVPVQLQSN 763  
Db 715 WEOTLPTLCEDPGAGVPRITLENVPLASPPKEDGEGASEENYVPVQLQSN 760

RESULT 5  
US-09-978-303-4  
; Sequence 4, Application US/09978303  
; Patent No. 6790629  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: Nucleic acid sequences encoding  
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related  
; TITLE OF INVENTION: polypeptides and uses thereof  
; FILE REFERENCE: UCAL084CON  
; CURRENT APPLICATION NUMBER: US/09/978,303

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; CURRENT FILLING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILLING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILLING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILLING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 761
; TYPE: PRT
; ORGANISM: R. rattus
; US-09-978-303-4

Query Match      76.2%; Score 3051.5; DB 4; Length 761;
Best Local Similarity 77.7%; Pred. No. 1.9e-278;
Matches 598; Conservative 62; Mismatches 93; Indels 17; Gaps 7;

QY 1 MTSPPSSPVRLTLDGGQEDGSEADRGKLDGSGLPPMESQFGEDRKFAFQIRVNLNY 60
Db 1 MTSASSPPAPRLTSDGDEGNAEVNKGQD-----PPMESPPQREDRNSSPQIKVNLNF 56
QY 61 ----RKG TGA- S QPDRNDRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYEGST 115
Db 57 IKRPPKNTSAPSQOEPRDRDRDLFVSVRGVPEELTGLLEYLRWNSKYLTDSEYEGST 116
QY 116 GKTCMKAVLNKXGQVNAACILPLLIQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRS 175
Db 117 GKTCMKAVLNKXGQVNAACIMPLLIQIDKDSGNPKPLVNAQCTDEFYQGHSAHIAIEKRS 176
QY 176 LQCVKLLVNGANVHARACGRPFQKGCGTCFYFGEPLSLAACTKQWDVVSYLENPHQP 235
Db 177 LQCVKLLVNGADVHLRACGRPFQKGCGTCFYFGEPLSLAACTKQWDVVSYLENPHQP 236
QY 236 ASLQATDSQNTVLHALVMTSDNSAENIALVTSMYDGLLQAGARLCTPTQLEDIRNLQDL 295
Db 237 ASLEATDSLNTVLHALVMTADNSPENSALVIHMYDGLLQAGARLCTPTQLEIRSHQGL 296
QY 296 TPLKAAKEGKIEIFRHILQREFSG-LSHLSRKFTWCYGPVRVSLYDLASVDSCENSV 354
Db 297 TPLKAAKEGKIEIFRHILQREFSGPVQPLSRKFTWCYGPVRVSLYDLSSVDSWEKNSV 356
QY 355 LEIIAFCKSPHRHVMVLEPLNKLQAKWDLLI PKFELFLNCLNYMFIFTAVAYHOPT 414
Db 357 LEIIAFCKSPHRHVMVLEPLNKLQAKWDRLVSRFFNFACVLYVMFIFTVAYHOQS 416
QY 415 LKQAAAPHLKAEVGNMMLTGHIILLGGIYLLVGOLWYFRRHVFITWISFYELLF 474
Db 417 LDQPALPSSKATFGESMLLGHILLGGIYLLQGLWYFRRRLFTWISFMDSYELLF 476
QY 475 LFOALLTWSQVLCFLAIEWYLPVLSALVGLNLLYYTRGFQHTGIYSVMTQKVLIR 534
Db 477 LQALLTVLSQVLRFMETEWYLPVLSVGLVGLNLLYYTRGFQHTGIYSVMTQKVLIR 536
QY 535 LIRPLLIYVFLFGFAVALVLSQEAWRPAPTGPKNATESVQPMQEGDEGNGAQYRGIL 594
Db 537 LIRPLLIYVFLFGFAVALVLSREARSPKAPEDNNSVTVEQPTVGQEEB--PAPYRSIL 594
QY 595 EASLELPKFTIGMGEALAFQBLFRGMVLLILLAYVLLTYLLINLIALMSTVNSVAT 654
Db 595 DASLELPKFTIGMGEALAFQBLFRGMVLLILLAYVLLTYLLINLIALMSTVNHAD 654
QY 655 DWSIWKLOKAI SVLEMENGYWC-RKKORAGVMLTVGTGKDS PDERMCFRVEEVNWA 713
Db 655 NWSIWKLOKAI SVLEMENGYWCCRKKHREGRLLVKVGTRGDGTPDERMCFRVEEVNWA 714
QY 714 WEOTLPTLCEDPSGAGVPTLENPVLASPKKEDGASENYVPVQLQS 763
Db 715 WEKTLPTLSBDSGPGTGNKNPT-----SKPGKNSASEEDHLPQVLQS 760

```

RESULT 6

```

US-09-235-451-23
; Sequence 23, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 727
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(727)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-235-451-23

Query Match      75.8%; Score 3036.5; DB 3; Length 727;
Best Local Similarity 79.1%; Pred. No. 4.6e-277;
Matches 620; Conservative 5; Mismatches 82; Indels 77; Gaps 10;

QY 1 MTSPPSSPVRLTLDGGQEDGSEADRGKLDGSGLPPMESQFGEDRKFAFQIRVNLNY 60
Db 1 MTSPPSSPVRLTLDGGQEDGSEADRGKLDGSGLPPMESQFGEDRKFAFQIRVNLNY 60
QY 61 RKGTCASQDPNDRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYEGSTGKTCL 120
Db 61 RKGTCASQDPNDRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYEGSTGKTCL 120
QY 121 MKAVLNKXGQVNAACILPLLIQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSIQCVK 180
Db 121 MKAVLNKXGQVNAACILPLLIQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSIQCVK 180
QY 181 LLVNGANVHARACGRPFQKGCGTCFYFGEPLSLAACTKQWDVVSYLENPHQASLOA 240
Db 181 LLVNGANVHARACGRPFQKGCGTCFYFGEPLSLAACTKQWDVVSYLENPHQASLOA 240
QY 241 TDSQNTVLHALVMTSDNSAENIALVTSMYDGLLQAGARLCTPTQLEDIRNLQDLTPLKL 300
Db 241 TDSQNTVLHALVMTSDNSAENIALVTSMYDGLLQAGARLCTPTQLEDIRNLQDLTPLKL 300
QY 301 AAKEGKIEIF-RHIL-QREFSGLS-HLSRKFTF-WCYGPVRVSLYDLASVDSCENSVLE 356
Db 301 AAKEGKIXIFXRHILASGKFGSLKPPFPRKFTEWMLMGVPRVXXXXXXXKXXXXXXX 360
QY 357 ITAFCKSPHRHVMVLEPLNKLQAKWDLLI PKFELFLNCLNYMFIFTAVAYHOPTLK 416
Db 361 XXXXXXXXDRHVMVLEPLNKLQAKWDLLI PKFELFLNCLNYMFIFTAVAYHOPTLK 420
QY 417 KQAAAPHLKAEVGNMMLTGHIILLGGIYLLVGOLWYFWR--HVF 460
Db 421 KQAAAPHLKAEVGNMMLTGHIILLGGIYLLVGOLWYFWR--HVF 478
QY 461 IWSIFDYSYEILFLFQALLTVVSQVLCFLAIEWYLPVLSALVGLNLLYYTRGFQHT 520
Db 479 -----RVVPAPACVCA---GAGLAEPALLYTWL-----PAHREL 509
QY 521 GIYSVMTQKVLIRDLRLFLIYVFLFGFAVALVLSQEAWRPAPTGPKNATESVQPMEG 580
Db 510 QCHD-----PEALVLSQD--WRPEAPTGPKNATESVQPMEG 543
QY 581 QDEGNGAQYRGILEASLELFTKFTIGMGEALAFQBLFRGMVLLILLAYVLLTYILLNM 640

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Db	544	QDEEGNGAQRGILXASLELFKFTTIGMGELAQEQQLHFRGMVLLLLLAAYVLLTYILLNNM	603
Qy	641	LIALMSETVNSVATDSWSIWKLQKAI SVLEMENGYWCRKKORAGVMLTVGTGKPDGSPDE	700
Db	604	LIALXSETVNSVATDSWSIWKLQKAI SVLEMENGYWCRKKORAGVMLTVGTGKPDGSPDE	663
Qy	701	RWCFRVEEVNWSWEOTLPTLCEDPGAGVPRTLNPNVLASPPKEDGASEENYVPVQL	760
Db	664	RWCFRVEEVNWSWEOTLPTLCEDPGAGVPRTLNPNVLASPPKEDGASEENYVPVQL	723
Qy	761	LQSN 764	
Db	724	LQSN 727	
RESULT 7			
US-09-978-303-23			
; Sequence 23, Application US/09978303			
; Patent No. 6790629			
; GENERAL INFORMATION:			
; APPLICANT: Julius, David J.			
; APPLICANT: Caterina, Michael J.			
; APPLICANT: Brake, Anthony J.			
; TITLE OF INVENTION: Nucleic acid sequences encoding			
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related			
; TITLE OF INVENTION: polypeptides and uses thereof			
; FILE REFERENCE: UCAL084CON			
; CURRENT APPLICATION NUMBER: US/09/978,303			
; CURRENT FILING DATE: 2001-10-15			
; PRIOR APPLICATION NUMBER: 09/235,451			
; PRIOR FILING DATE: 1999-01-22			
; PRIOR APPLICATION NUMBER: 60/072,151			
; PRIOR FILING DATE: 1998-01-22			
; PRIOR APPLICATION NUMBER: 08/915,461			
; PRIOR FILING DATE: 1997-08-20			
; NUMBER OF SEQ ID NOS: 48			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 23			
; LENGTH: 727			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: VARIANT			
; LOCATION: (1)...(727)			
; OTHER INFORMATION: Xaa = Any Amino Acid			
US-09-978-303-23			
Query Match 75.8%; Score 3036.5; DB 4; Length 727;			
Best Local Similarity 79.1%; Pred. No. 4.6e-277;			
Matches 620; Conservative 5; Mismatches 82; Indels 77; Gaps 10;			
Qy	1	MTSPSSGFVFRLETLDDGQEDGSEADRGKLDGFGSLPPMESQFGEDRKFAPIRVNLNY	60
Db	1	MTSPSSGFVFRLETLDDGQEDGSEADRGKLDGFGSLPPMESQFGEDRKFAPIRVNLNY	60
Qy	61	RKGTGASQPDNRRDRDLFNAVRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGTCL	120
Db	61	RKGTGASQPDNRRDRDLFNAVRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGTCL	120
Qy	121	MKAVNLKQGNACILPLQIDRDSGNPQPLVNAQCTDDYYRGSHALHIAIEKRSLOCVK	180
Db	121	MKAVNLKQGNACILPLQIDRDSGNPQPLVNAQCTDDYYRGSHALHIAIEKRSLOCVK	180
Qy	181	LLVENGANVHARACGRFPQGGTCFVFGELPLSLAACKTQWDVVSYLENPHQPASLOA	240
Db	181	LLVENGANVHARAXXXXXXXXXXXXXXXXXXGELPLSLAACKTQWDVVSYLENPHQPASLOA	240
Qy	241	TDSQNTVLHALVMSDMSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPKL	300
Db	241	TDSQNTVLHALVMSDMSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPKL	300
Qy	301	AAEGKIEIF-RHIL-QREFSGLS-HLSRKETE-WCYGPVRVSLYDLASVDSCEENSYLE	356
US-09-235-451-25			
; Sequence 25, Application US/09235451			
; GENERAL INFORMATION:			
; APPLICANT: Julius, David J.			
; APPLICANT: Caterina, Michael J.			
; APPLICANT: Brake, Anthony J.			
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING			
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED			
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF			
; FILE REFERENCE: 9076/084CIP			
; CURRENT APPLICATION NUMBER: US/09/235,451			
; CURRENT FILING DATE: 1999-01-22			
; PRIOR APPLICATION NUMBER: 60/072,151			
; PRIOR FILING DATE: 1998-01-22			
; PRIOR APPLICATION NUMBER: 08/915,461			
; PRIOR FILING DATE: 1997-08-20			
; NUMBER OF SEQ ID NOS: 48			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 25			
; LENGTH: 843			
; TYPE: PRT			
; ORGANISM: chicken			
US-09-235-451-25			
Query Match 42.2%; Score 1689; DB 3; Length 843;			
Best Local Similarity 47.2%; Pred. No. 6.4e-150;			
Matches 358; Conservative 118; Mismatches 218; Indels 64; Gaps 12;			
Qy	4	PSSSPVFRLETLDDGQEDGSEADRGKL---DFGSLPPMESQFGEDRKFAPO-IRVNLN	59
Db	49	PSKSNIF-----ARRGRFVMGDCDKMAPMDSFYQ-MDHLMAPSVIKPHAN	93
Qy	60	YRKG-----TCASQPDNRRDRDLFNAVRGVPEDLAGLPEYLSKTSKYLTD	108
Db	94	MERGKHLKLLSTDSITGCSKAFKFYDRRRIFDAVARGSTKDLDDLLLYLNRTLKHLTDD	153

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QY 109 EYTEGSTGCTCKMLKAVLNKDGYNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALH 168
Db 154 EFKEPBTGKTCLUKAMLNLDHGKNDTIPLLDDIAKKTGTGLKEFVNAEYTDNYTKGQTALH 213
QY 169 IATIEKRSLOCVKLLVNGANVHARACGRFFQKQG--TCFYFGEPLPLSLAACTKQMDVWSY 227
Db 214 IAIERNMVLVLLVQNGADVHARACGEFFRKIKGKPGFYFGEPLPLSLAACTNQLCIVKF 273
QY 228 LLENPHQASLQATDSQNTVLHALVMSDNSAENIALVTSMDGLLQAGARLCPVQLE 287
Db 274 LLENPYQAADIAAEDSMGNMVLHTLVEIADNTKDTKFTVMNNILILGAKINPLKLE 333
QY 288 DIRNLQDLPLKAAKEGKIEIFRHILQREFSG--LSHLSRKFTWCYGPVRVSLYDLAS 345
Db 334 ELTNKKGLTPLTAAKTGKIGIPAYILRREIKDPCRHSRKFTWAYGPGVHSSLYDLS 393
QY 346 VDSCEENSLEIITAFHCKSPHRRMVVLEPLNKLQAKWDLLIPK--FFLNFCLNLIYMPI 404
Db 394 IDTCEKNSVLEIITAYSETPNRHEMLLVPEPLNLLQDKWDRFVKHLFYFNFFVYAIHISI 453
QY 405 FTAVAYHOPTLKKQAAPH--LKAEVGNSMLLTGHILILGGIYLLVQGLWYFWRHVFIMI 463
Db 454 LTTAAAYRVPVKGDKEPPFAFGHSTGEYFRVTGEILSVLGLYFFFRGIQYFVQRRPSLKT 513
QY 464 SFIDSYPEILFQALLTVVSOVLCLAEWYLPLLVSAVLGMLNLLYYTRGFOHTGIY 523
Db 514 LIVDSYSEVLFFVHSLLSLVVLYFCGOELVYASVMSLALGANMMLYYTRGFOOMGIY 573
QY 524 SVMIOKVILRLRFLLIYVFLGFAVALVSLSQEAWRPEAPTGNATESVQPMEGQD 583
Db 574 SVMIAKMILRDLCRFMFVYVLLGFGSTAVVTLIED-----DNEGQDT 616
QY 584 EGN-----GAQYRGILEASLELPKFTTGMGELAPQBLHFRGMVLLLLAYVLL 632
Db 617 NSSEYARCSHTKRGRTSYNSLYYTCLLEPKFTTGMGDLFTENYRFKSVFVILLVYL 676
QY 633 TYILLANMLIALMSETVNSVATDSIWKLQAKAISVLEMENGYWVC--RKKORAGVMLTVG 691
Db 677 TYILLANMLIALMGETVSKIAQESKIWKLQRPITLIDENSYLNCRLRSRGRKRVLVG 736
QY 692 TKPDGSPDERWCFRVEEVNWSWEQTLPTLCEDPSGAG 729
Db 737 ITPDGQDDYRWCFRVDENVNWSWTNLTNLGIINEDPGCSG 774
```

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RESULT 9
US-09-978-303-25
; Sequence 25, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 843
; TYPE: PRT
; ORGANISM: chicken
US-09-978-303-25
```

```
Query Match 42.2%; Score 1689; DB 4: Length 843;
Best Local Similarity 47.2%; Pred. No. 6.4e-150;
Matches 358; Conservative 118; Mismatches 218; Indels 64; Gaps 12;

QY 4 PSSSPVFRLETLDCGQEDGSEADRGKL---DFGSGLPMPMESQFQGEDRKFAPQ--IRVNIN 59
Db 49 PSKSNIF-----ARRGRFVWGDCDKMAPDMSFYQ--MDHLMARSVIKFHFAN 93
QY 60 YRKG-----TGASQDPNRPDRDLRFNAVSRGVPEDLAGLPEYLSKTSKYLTS 108
Db 94 MERGKHLKLLSDTSITGCSKAFKFEYDRRIIFDAVARGSTKDDLLLLYINRTHLHTDD 153
QY 109 EYTEGSTGCTCKMLKAVLNKDGYNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALH 168
Db 154 EFKEPBTGKTCLUKAMLNLDHGKNDTIPLLDDIAKKTGTGLKEFVNAEYTDNYTKGQTALH 213
QY 169 IATIEKRSLOCVKLLVNGANVHARACGRFFQKQG--TCFYFGEPLPLSLAACTKQMDVWSY 227
Db 214 IAIERNMVLVLLVQNGADVHARACGEFFRKIKGKPGFYFGEPLPLSLAACTNQLCIVKF 273
QY 228 LLENPHQASLQATDSQNTVLHALVMSDNSAENIALVTSMDGLLQAGARLCPVQLE 287
Db 274 LLENPYQAADIAAEDSMGNMVLHTLVEIADNTKDTKFTVMNNILILGAKINPLKLE 333
QY 288 DIRNLQDLPLKAAKEGKIEIFRHILQREFSG--LSHLSRKFTWCYGPVRVSLYDLAS 345
Db 334 ELTNKKGLTPLTAAKTGKIGIPAYILRREIKDPCRHSRKFTWAYGPGVHSSLYDLS 393
QY 346 VDSCEENSLEIITAFHCKSPHRRMVVLEPLNKLQAKWDLLIPK--FFLNFCLNLIYMPI 404
Db 394 IDTCEKNSVLEIITAYSETPNRHEMLLVPEPLNLLQDKWDRFVKHLFYFNFFVYAIHISI 453
QY 405 FTAVAYHOPTLKKQAAPH--LKAEVGNSMLLTGHILILGGIYLLVQGLWYFWRHVFIMI 463
Db 454 LTTAAAYRVPVKGDKEPPFAFGHSTGEYFRVTGEILSVLGLYFFFRGIQYFVQRRPSLKT 513
QY 464 SFIDSYPEILFQALLTVVSOVLCLAEWYLPLLVSAVLGMLNLLYYTRGFOHTGIY 523
Db 514 LIVDSYSEVLFFVHSLLSLVVLYFCGOELVYASVMSLALGANMMLYYTRGFOOMGIY 573
QY 524 SVMIOKVILRLRFLLIYVFLGFAVALVSLSQEAWRPEAPTGNATESVQPMEGQD 583
Db 574 SVMIAKMILRDLCRFMFVYVLLGFGSTAVVTLIED-----DNEGQDT 616
QY 584 EGN-----GAQYRGILEASLELPKFTTGMGELAPQBLHFRGMVLLLLAYVLL 632
Db 617 NSSEYARCSHTKRGRTSYNSLYYTCLLEPKFTTGMGDLFTENYRFKSVFVILLVYL 676
QY 633 TYILLANMLIALMSETVNSVATDSIWKLQAKAISVLEMENGYWVC--RKKORAGVMLTVG 691
Db 677 TYILLANMLIALMGETVSKIAQESKIWKLQRPITLIDENSYLNCRLRSRGRKRVLVG 736
QY 692 TKPDGSPDERWCFRVEEVNWSWEQTLPTLCEDPSGAG 729
Db 737 ITPDGQDDYRWCFRVDENVNWSWTNLTNLGIINEDPGCSG 774
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RESULT 10
US-09-235-451-2
; Sequence 2, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
```

; PRIOR FILING DATE: 1997-08-20  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 838  
 ; TYPE: PRT  
 ; ORGANISM: R. rattus  
 ; US-09-235-451-2

Query Match 41.3%; Score 1652; DB 3; Length 838;  
 Best Local Similarity 46.3%; Pred. No. 1.9e-146;  
 Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;

Qy	18	GOEDGSEADRGKLDGSGGLPPMESQFQEDRKFAPOIRVN---	LNYRKGTG-----	65
Db	51	GKGDSEAS-----	PLDCPYEEGGLASCPITVSSVLTIQRPDGPASVRPSQ	99
Qy	66	-----ASQPDNPRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTSEYTEGSGTKTCLM	121	
Db	100	DSVSAGEKPRLYDRRSIFDAVAQNCQELSLPLFLQSKKRLTDFEFKDPETGKTCLL	159	
Qy	122	KAVLNKDGVNACILPLQIDRDSGNPQPLVNAQCTDDYVGHSAHIAIEKSLQCVKL	181	
Db	160	KAMLNHNGQNDTIALLDVARKTSLKQFVNASYTDSYKGTALHIAIERNNMTLVLT	219	
Qy	182	LVENGANVHARACGRPFQKQGG--TCFYFGEPLPLSLAACTQMDVSWSYLLENPHQPASLOA	240	
Db	220	LVENGADVQAANGDFPKTKGRPGFYFGEPLPLSLAACTNQLAIVKFLQNSWQPADISA	279	
Qy	241	TDSQGNVTLHALVMSIDNSAENIALVTSYDGLLOAGARLCPTVQLIEDIRNLDLPLKL	300	
Db	280	RDSVGNVTLHALVEADVNTVDNTKFTVSMYNEILILGAKLHPTLKEEITNRKGLTFLAL	339	
Qy	301	AKEGKTEIPIRHILQREF--SGLSHLSRKTEWCYGPVRVSLYDLASVDSCEANSVLEII	358	
Db	340	AASGKIGVLAYILQREIHEPECRHLSRKTEWAYGPHVSHSLYDLSCIDTCEKNSVLEVI	399	
Qy	359	AP-HCKSPHRRMVLEPLNKLQAKWDLIPK--FFLNFLCNLIYMFIFTAVAYHOPTLK	416	
Db	400	AYSSETPNRHDMLLVPELNRLQDKWDRFVKRIFNFYFVCLYMIIFTAAAYRPV--	457	
Qy	417	KQAAP--HLKAEVGNMMLTGHILILGGLIYLLVQGLWYFWRHVFIIWISFIDSYEILF	474	
Db	458	-EGLPPYKLNVTGDIYFRVTGEILSVSGGYVFFRGIQYFLQRRPSLSLFDVSYSEILF	516	
Qy	475	LFQALLTVVSQVLCFLAIEWYLPVLSALVGLWNLNLYYTRGQHTGIYSVMIOKVILRD	534	
Db	517	FVQSLFVLVSVLYFSQKEYVASMVFLSANGMTNMLYYTRGQOMGIYAVMIEKMLRD	576	
Qy	535	LRPLLIYVFLFGFVALVSLSQEAWRPEAPTGNATESVQPMQEGDESGNCA-----	588	
Db	577	LCRPFMYLVFLFGFSTAVVTLIED-----GKN---NSLPMESTPHKCRSACKPGN	625	
Qy	589	QYRGILEASLELPKFTIGMGELEAFQOLHFRGMVLLLLAYVLLTYTILLNMLIALMSET	648	
Db	626	SYNSLYSTCLELFPKFTIGMGELEAFQOLHFRGMVLLLLAYVLLTYTILLNMLIALMSET	685	
Qy	649	VNSVATDSWSIWLQKAIISVLEMGYWWC--RKQKAGVMTLVGTGPDGSPDRCWCRVE	707	
Db	686	VNKIAQESKNIKWLQRAITILDTKESFLKCMKRAFRSGKLLQVGTTPDGKDDYRWCPRVD	745	
Qy	708	EWNWASWEQTLPTLCEDPSGA--GVPRTLENPVLASPPKEDGSEBENYVVPOLLQ	762	
Db	746	EVNWTNTNVTNVTIINEDPGNCEGVKRTLSFSLRSG-----RVSGRNWKNFALVPLLR	797	

RESULT 11  
 US-09-132-316-3  
 ; Sequence 3, Application US/09132316B  
 ; Patent No. 644440  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Paul E.  
 ; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Vanilloid Receptor-2  
 ; FILE REFERENCE: 1488.1110000  
 ; CURRENT APPLICATION NUMBER: US/09/132,316B  
 ; CURRENT FILING DATE: 1998-08-11  
 ; EARLIER APPLICATION NUMBER: US 60/040,163  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493  
 ; EARLIER FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 67  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 838  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 ; US-09-132-316-3

Query Match 41.3%; Score 1652; DB 4; Length 838;  
 Best Local Similarity 46.3%; Pred. No. 1.9e-146;  
 Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;

Qy	18	GOEDGSEADRGKLDGSGGLPPMESQFQEDRKFAPOIRVN---	LNYRKGTG-----	65
Db	51	GKGDSEAS-----	PLDCPYEEGGLASCPITVSSVLTIQRPDGPASVRPSQ	99
Qy	66	-----ASQPDNPRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTSEYTEGSGTKTCLM	121	
Db	100	DSVSAGEKPRLYDRRSIFDAVAQNCQELSLPLFLQSKKRLTDFEFKDPETGKTCLL	159	
Qy	122	KAVLNKDGVNACILPLQIDRDSGNPQPLVNAQCTDDYVGHSAHIAIEKSLQCVKL	181	
Db	160	KAMLNHNGQNDTIALLDVARKTSLKQFVNASYTDSYKGTALHIAIERNNMTLVLT	219	
Qy	182	LVENGANVHARACGRPFQKQGG--TCFYFGEPLPLSLAACTQMDVSWSYLLENPHQPASLOA	240	
Db	220	LVENGADVQAANGDFPKTKGRPGFYFGEPLPLSLAACTNQLAIVKFLQNSWQPADISA	279	
Qy	241	TDSQGNVTLHALVMSIDNSAENIALVTSYDGLLOAGARLCPTVQLIEDIRNLDLPLKL	300	
Db	280	RDSVGNVTLHALVEADVNTVDNTKFTVSMYNEILILGAKLHPTLKEEITNRKGLTFLAL	339	
Qy	301	AKEGKTEIPIRHILQREF--SGLSHLSRKTEWCYGPVRVSLYDLASVDSCEANSVLEII	358	
Db	340	AASGKIGVLAYILQREIHEPECRHLSRKTEWAYGPHVSHSLYDLSCIDTCEKNSVLEVI	399	
Qy	359	AP-HCKSPHRRMVLEPLNKLQAKWDLIPK--FFLNFLCNLIYMFIFTAVAYHOPTLK	416	
Db	400	AYSSETPNRHDMLLVPELNRLQDKWDRFVKRIFNFYFVCLYMIIFTAAAYRPV--	457	
Qy	417	KQAAP--HLKAEVGNMMLTGHILILGGLIYLLVQGLWYFWRHVFIIWISFIDSYEILF	474	
Db	458	-EGLPPYKLNVTGDIYFRVTGEILSVSGGYVFFRGIQYFLQRRPSLSLFDVSYSEILF	516	
Qy	475	LFQALLTVVSQVLCFLAIEWYLPVLSALVGLWNLNLYYTRGQHTGIYSVMIOKVILRD	534	
Db	517	FVQSLFVLVSVLYFSQKEYVASMVFLSANGMTNMLYYTRGQOMGIYAVMIEKMLRD	576	
Qy	535	LRPLLIYVFLFGFVALVSLSQEAWRPEAPTGNATESVQPMQEGDESGNCA-----	588	
Db	577	LCRPFMYLVFLFGFSTAVVTLIED-----GKN---NSLPMESTPHKCRSACKPGN	625	
Qy	589	QYRGILEASLELPKFTIGMGELEAFQOLHFRGMVLLLLAYVLLTYTILLNMLIALMSET	648	
Db	626	SYNSLYSTCLELFPKFTIGMGELEAFQOLHFRGMVLLLLAYVLLTYTILLNMLIALMSET	685	
Qy	649	VNSVATDSWSIWLQKAIISVLEMGYWWC--RKQKAGVMTLVGTGPDGSPDRCWCRVE	707	
Db	686	VNKIAQESKNIKWLQRAITILDTKESFLKCMKRAFRSGKLLQVGTTPDGKDDYRWCPRVD	745	
Qy	708	EWNWASWEQTLPTLCEDPSGA--GVPRTLENPVLASPPKEDGSEBENYVVPOLLQ	762	
Db	746	EVNWTNTNVTNVTIINEDPGNCEGVKRTLSFSLRSG-----RVSGRNWKNFALVPLLR	797	



QY 417 KOAAP--HLKAEYNGSMLLTGHILILGGLIYLLVGLQWTFWRRHVFIMTSDSYPEILF 474  
DB 458 -EGLPPYKLNVTGDFRVTVGTEILSVGGVYFFRGIOYFLQRRPSLKSFLVDSYSEILF 516  
QY 475 LFOALTVVSQVLCFLAIEWYLLPVLVSALVGLWNLVYTRGPHQHTGIYSVMIKVILRD 534  
DB 517 FVQSLFMLSVLVYFSQRKEYVASMVFSLWGTNMLVYTRGPHQHTGIYSVMIKVILRD 576  
QY 535 LLRFLIYLVPLFGFAVALVLSQEAWRPEAPTGPNTATESVQPMQOEDEGNA----- 588  
DB 577 LCRFMPYVFLFPGFSTAVVTLIED-----GKN-----NSLPWESTPHKRCGSACKPGN 625  
QY 589 QYRGILEASLELKFPTIGMELAFQOLHFRGMVLLLLAYVLLTYLLINMLIALMSET 648  
DB 626 SYNSLSTCLELKFPTIGMGLTEFTENYDFKAVFIILLAYVILTYLLINMLIALMSET 685  
QY 649 VNSVATDSMSIWKLOKAIISVLEMGYWC-RKKORAGVNLTVGTGPDGSPDERWCFRVE 707  
DB 686 VNKIAQESKNIKLQRAITILDTEKSPKCMKRAFRSGKLLQVGTGPDGKDDYRWCPRVD 745  
QY 708 EVNWASHEQTLPTLCEDPSGA-GVPRITLENPVLASPPKEDGASBENTYVPVOLLQ 762  
DB 746 EVNWTTNTVNGIINEDPGNCEGVKRTLSFSLRSG-----RVSGRNWKNFALVPLLR 797

## RESULT 14

US-09-667-422-4  
; Sequence 4, Application US/09667422  
; Patent No. 6482611  
; GENERAL INFORMATION:  
; APPLICANT: Cortright, Daniel  
; APPLICANT: Krause, James  
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof  
; FILE REFERENCE: HCR  
; CURRENT APPLICATION NUMBER: US/09/667,422  
; CURRENT FILING DATE: 2001-06-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 839

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: TRANSMEM

LOCATION: (434)..(455)

OTHER INFORMATION: TM1

NAME/KEY: TRANSMEM

LOCATION: (480)..(495)

OTHER INFORMATION: TM2

NAME/KEY: TRANSMEM

LOCATION: (510)..(530)

OTHER INFORMATION: TM3

NAME/KEY: TRANSMEM

LOCATION: (543)..(569)

OTHER INFORMATION: TM4

NAME/KEY: TRANSMEM

LOCATION: (577)..(596)

OTHER INFORMATION: TM5

NAME/KEY: TRANSMEM

LOCATION: (656)..(684)

OTHER INFORMATION: TM6

US-09-667-422-4

Query Match 41.2%; Score 1651.5; DB 4; Length 839;  
Best Local Similarity 48.5%; Pred. No. 2.2e-146;  
Matches 344; Conservative 122; Mismatches 199; Indels 45; Gaps 11;

QY 74 FDRDLFNASRGVPELAGLPEYLSKTSKYLTDSYBTEGSTGKTCMLKAVNLKDGVA 133

DB 113 YDRSIFEAVANNQDLESLLFLQSKKHLLTDFNEFKDPTGKTKLLKAMNLHDGNT 172

QY 134 CILPLQLDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSQCCKLVGVANGVHARA 193

DB 173 TIPLLEIARQTDSEKELVNASYTDYKYGQTAHIAIBERNMALVTLVENGADVQAAA 232  
QY 194 CRRFFQKQG--TCFYFGLPLSLAACTKQMDVVSVLLENPHOPASLOATDSQNTVLHAL 252  
DB 233 HDGFKKYKRGPCFFGELPLSLAACTNQLGIVKVELLQNSWTADISARDSVGNVTLHAL 292  
QY 253 VMSDNSAENIALVTSMDYGLLOAGARLCPTVOLEDIRNLQDLTPUKLAAGKGIKIFRH 312  
DB 293 VEADVNTADNTKFTVSMYNEILLMGLAKHPTLKLBELTNKKGMTPLALAAGTGKIGVLA 352  
QY 313 ILORFES--GLSHLSRKFTWCYGPVRSVLYDLASVDSCEENSVLRIIAF-HCKSPHRHR 369  
DB 353 ILQRIQIEPECRLSKRFTWYAGPVHSSLYDLSCIDTCEKNSVLEIVAYSSETPNRHD 412  
QY 370 MVVLEPLNKLQAKDMLLPK--FFLNFLCNLYMFIETAVAYHQPITLKKQAAAPHLKAE-V 427  
DB 413 MLVLEPLNKLQAKDMLLPK--FFLNFLCNLYMFIETAVAYHQPITLKKQAAAPHLKAE-V 469  
QY 428 GNSMLTGHILILGGLIYLLVGLQWTFWRRHVFIMTSDSYPEILFQALTVVSQVIL 487  
DB 470 GDVFRVTGBILSVLGGVYFFRGIOYFLQRRPSMKTFLVDSYSEMLFFLQSLFMLATVVL 529  
QY 488 CFLATEWYLLPVLVSALVGLWNLVYTRGPHQHTGIYSVMIKVILRDLLRFLIYLVFLF 547  
DB 530 YFSLHKEYVASMVFSLWGTNMLVYTRGPHQHTGIYSVMIKVILRDLLRFLIYLVFLF 589  
QY 548 GFPAVALVLSQEA-----WRPEAPTGPNTATESVQPMQOEDEGNAQYRGIL 594  
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QY 595 EASLELKFPTIGMELAFQOLHFRGMVLLLLAYVLLTYLLINMLIALMSETVNSVAT 654  
DB 633 STCLELKFPTIGMGLTEFTENYDFKAVFIILLAYVILTYLLINMLIALMSETVNSVAT 692  
QY 655 DWSIWKLOKAIISVLEMGYWC-RKKORAGVNLTVGTGPDGSPDERWCFRVEENWAS 713  
DB 693 ESKNIWKLOKAIISVLEMGYWC-RKKORAGVNLTVGTGPDGSPDERWCFRVEENWAS 752  
QY 714 WEQTLPTLCEDPSGA-GVPRITLENPVLASPPKEDGASBENTYVPVOLLQ 762  
DB 753 WNTVNGIINEDPGNCEGVKRTLSFSLRSG-----RVSGRNWKNFALVPLLR 798

## RESULT 15

US-09-197-636-2  
; Sequence 2, Application US/09197636  
; Patent No. 6239267  
; GENERAL INFORMATION:  
; APPLICANT: DUCKWORTH, DAVID  
; APPLICANT: HAYES, PHILIP  
; APPLICANT: MEADOWS, HELEN  
; APPLICANT: DAVIS, JOHN  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ratner & Prestia  
; STREET: P.O. Box 980  
; CITY: Valley Forge  
; STATE: PA  
; COUNTRY: US  
; ZIP: 19482-0980  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/197,636  
; FILING DATE: 23-NOV-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 9805137.8



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QM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:51:46 ; Search time 1573 Seconds  
(without alignments)  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482402727 residues 16886260

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Maximum Match 100%  
Listing first 45 summaries

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25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:  
26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2462.2	99.7	2809	19	US-10-757-262-25
2	2462.2	99.7	2809	24	US-11-013-090-4
3	2455.8	99.5	2825	16	US-10-168-651-30
4	2447.4	99.1	2867	17	US-10-264-237-1401
5	2424.6	98.2	2805	14	US-10-137-316-1
6	2378.4	96.3	2380	10	US-09-978-303-35
7	2378.4	96.3	2380	21	US-10-915-017-35

8	2293.4	92.9	2295	17	US-10-342-844-67	Sequence 67, Appl
9	2292	92.8	2292	24	US-11-013-090-6	Sequence 6, Appl
10	2263.2	91.7	2295	17	US-10-342-844-69	Sequence 69, Appl
11	2259.2	91.5	2779	10	US-09-809-391-191	Sequence 191, Appl
12	2259.2	91.5	2779	10	US-09-882-171-191	Sequence 191, Appl
13	2259.2	91.5	2779	17	US-10-164-861-191	Sequence 191, Appl
14	2061.8	83.5	2860	10	US-09-809-391-314	Sequence 314, Appl
15	2061.8	83.5	2860	10	US-09-882-171-314	Sequence 314, Appl
16	2061.8	83.5	2860	17	US-10-164-861-314	Sequence 314, Appl
17	1933.4	78.3	1935	17	US-10-342-844-43	Sequence 43, Appl
18	1572	63.7	2824	21	US-10-764-420-2281	Sequence 2281, Appl
19	1535.8	62.2	2271	17	US-10-342-844-51	Sequence 51, Appl
20	1529.4	61.9	2271	17	US-10-342-844-85	Sequence 85, Appl
21	1522.4	61.7	2736	21	US-09-978-303-3	Sequence 3, Appl
22	1522.4	61.7	2736	21	US-10-915-017-3	Sequence 3, Appl
23	1459.6	59.1	2286	17	US-10-342-844-45	Sequence 45, Appl
24	1458	59.1	2286	17	US-10-342-844-33	Sequence 33, Appl
25	1445.6	58.6	2289	17	US-10-342-844-97	Sequence 97, Appl
26	1098.4	44.5	1794	24	US-11-013-090-10	Sequence 10, Appl
27	1065.8	43.2	1662	24	US-11-013-090-12	Sequence 12, Appl
28	1007.4	40.8	1489	24	US-11-013-090-7	Sequence 7, Appl
29	1005.4	40.7	1308	24	US-11-013-090-9	Sequence 9, Appl
30	750.8	30.4	884	10	US-09-978-303-22	Sequence 22, Appl
31	750.8	30.4	884	21	US-10-915-017-22	Sequence 22, Appl
32	711	28.8	876	10	US-09-809-391-315	Sequence 315, Appl
33	711	28.8	876	10	US-09-882-171-315	Sequence 315, Appl
34	711	28.8	876	17	US-10-164-861-315	Sequence 315, Appl
35	675.4	27.4	891	21	US-10-479-081-7	Sequence 7, Appl
36	662.4	26.8	2517	24	US-11-013-090-3	Sequence 3, Appl
37	662.4	26.8	2520	17	US-10-342-844-47	Sequence 47, Appl
38	662.4	26.8	2520	17	US-10-342-844-73	Sequence 73, Appl
39	662.4	26.8	2520	17	US-10-342-844-81	Sequence 81, Appl
40	662.4	26.8	3261	17	US-10-191-997-120	Sequence 120, Appl
41	662.4	26.8	3909	24	US-11-013-090-1	Sequence 1, Appl
42	662.4	26.8	4182	14	US-10-246-435-2	Sequence 2, Appl
43	662.4	26.8	4203	14	US-10-246-435-1	Sequence 1, Appl
44	660.8	26.8	2520	17	US-10-342-844-41	Sequence 41, Appl
45	660.8	26.8	2544	10	US-09-978-303-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1  
US-10-757-262-25  
; Sequence 25, Application US/10757262  
; Publication No. US20040197825A1  
; GENERAL INFORMATION:  
; APPLICANT: Karicheti, Venkateswarlu  
; APPLICANT: Silos-Santiago, Immaculada  
; APPLICANT: Eliasof, Scott D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884, 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047, 33751, 52872, 14063, 20739, 32544, 43239, 51164, 33751, 52872, 1587, 2207, 22245, 2387, 52908, 69112, 14990, 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990, 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675, 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423, 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643, 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR  
; TITLE OF INVENTION: 55053  
; FILE REFERENCE: MPI03-007P1RNMNMIM  
; CURRENT APPLICATION NUMBER: US/10757,262  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 60/440,318  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/444,783  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/457,901  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/468,775  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/471,614

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; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 2809
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (361)...(2655)
; US-10-757-262-25

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2464; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB      |
QY      327 TCCTGGCTGACCGAGGAGCCTCTCTCTAGATGACCTCAACCTCCAGCTCTCCAGT 386
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QY      363 GGAATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACAGCAAGTACTCAACGACTCGGA 422
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QY      687 ATACACAGAGGGCTCCACAGGTAAGAGTCCCTGATGAGAGGCTGTGCTGAACCTTAAGGA 746
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QY      603 CGCCATTGAGAGAGGAGTCTGACGTGTGTAAGACTCTCGTGAGAGTAATGGGGCCCAATGT 662
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QY      867 CGCCATTGAGAGAGGAGTCTGACGTGTGTAAGACTCTCGTGAGAGTAATGGGGCCCAATGT 926
DB      |
QY      663 GCATGCCCGGGCTGCGGGCGCTTCTTCCAGAGAGGGCCAAAGGAGCTTGTCTTTTATTCGG 722
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QY      927 GCATGCCCGGGCTGCGGGCGCTTCTTCCAGAGAGGGCCAAAGGAGCTTGTCTTTTATTCGG 986
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QY      1047 GGAGAAACCCACACACAGCCCGCAGCTGCAGGCCACTGACTCCAGGGGCAACACAGTCTCT 1106
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QY      843 GCATGCCCTAGTGTGATGATCTCGGACAACTCAGCTGAGAACTGTCATCTGTCAGCAGCAT 902
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QY      903 GTATGATGGGCTCTCTCAAGCTGGGGCCGCTCTGCCCTTACCTGTCAGCTGTCAGCAGCAT 962
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QY      1407 TGAGAGAACTCAGTGTCTGAGATCATTTGCCCTTTTATTGCAAGAGCCCGCACCGAC 1466
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QY      1203 AATGTCGTTTTGGAGCCCTGAAACAACTGTGTCAGGCGAAATGGGATCTGCTCATGCC 1262
DB      |
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DB      |
QY      1263 CAAGTCTTTTAAACTTCTGTGTAATCTGATCTACATGTTTCATCTTCCAGCTCTGTC 1322
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QY      1527 CAAGTCTTTTAAACTTCTGTGTAATCTGATCTACATGTTTCATCTTCCAGCTCTGTC 1586
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QY      1323 CTACCATCAGCTTACCTGAAAGCAGGCGCCCTCACCTGAAAGCGAGGTTGGAAA 1382
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QY      1587 CTACCATCAGCTTACCTGAAAGCAGGCGCCCTCACCTGAAAGCGAGGTTGGAAA 1646
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QY      1383 CTTCATGCTGTGACGGGCCAATCTCTTATCTGTGAGGGGGAATCTA CTTCTCTGTGG 1442
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QY      1707 CCAGCTGTGTTACTTCTGGCGGCGCACGTTTCATCTCGATCTCGTTTCATAGACAGCTA 1766
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QY      1503 CTTTGAATTCCTCTTCTGTTCCAGGCCCTGCTCA CAGTGTGTCTCCAGGTGTGTGTTT 1562
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QY      1563 CTTGGCCATCGAGTGTGTA CTTGCCCCCTGTGTGTCGCTGTGTCGTCGGCTGGCTGAA 1622
DB      |
QY      1827 CTTGGCCATCGAGTGTGTA CTTGCCCCCTGTGTGTCGCTGTGTCGTCGGCTGGCTGAA 1886
DB      |
QY      1623 CTTGCTTTTACTATACAGTGGCTTCCAGCACACAGGCACTTACAGTGTCTATGATCCAGAA 1682
DB      |
QY      1887 CTTGCTTTTACTATACAGTGGCTTCCAGCACACAGGCACTTACAGTGTCTATGATCCAGAA 1946
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QY      1683 GGTTCATCTCGGGACCTCTGCGCTTCTTCTGATCTTACTTACTTCTTCTTTCGGCTT 1742
DB      |
QY      1947 GGTTCATCTCGGGACCTCTGCGCTTCTTCTGATCTTACTTACTTCTTCTTTCGGCTT 2006
DB      |
QY      1743 CGCTGTAGCCCTGTGTGAGCCTTGAGCCAGGAGCTTGGCGCCCGAAAGCTTCTTACAGGCC 1802
DB      |
QY      2007 CGCTGTAGCCCTGTGTGAGCCTTGAGCCAGGAGCTTGGCGCCCGAGAGCTTCTTACAGGCC 2066
DB      |
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QY 1803 CAATGCACAGAGTCAGTGCAGCCCATGGAGGACAGAGGCAACGGGGCCCA 1862
Db 2067 CAATGCCACAGAGTCAGTGCAGCCCATGGAGGACAGAGGCAACGGGGCCCA 2126
QY 1863 GTACAGGGGATCCTGGAGCCCTCTTGGAGCTCTTCAAATTCACATCGCATGGGCGA 1922
Db 2127 GTACAGGGGATCCTGGAGCCCTCTTGGAGCTCTTCAAATTCACATCGCATGGGCGA 2186
QY 1923 GCTGGCTTCCAGGAGCAGTGCACATTCGCGGCATGGTCTGCTGCTGCTGCTGCTA 1982
Db 2187 GCTGGCTTCCAGGAGCAGTGCACATTCGCGGCATGGTCTGCTGCTGCTGCTGCTA 2246
QY 1983 CGTGTGCTCACCTACATCTGCTGCTCAACATGCTCATCGCCCTCATGAGCAGACCGT 2042
Db 2247 CGTGTGCTCACCTACATCTGCTGCTCAACATGCTCATCGCCCTCATGAGCAGACCGT 2306
QY 2043 CAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCGAAGGCCATCTCTGCTCT 2102
Db 2307 CAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCGAAGGCCATCTCTGCTCT 2366
QY 2103 GGAGATGGAGATGGCTATTGGTGTGCGAGGAGAGCAGCGGCGAGGTGTGATGCTGAC 2162
Db 2367 GGAGATGGAGATGGCTATTGGTGTGCGAGGAGAGCAGCGGCGAGGTGTGATGCTGAC 2426
QY 2163 CGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGCTTCAAGGCTGAGGAGGT 2222
Db 2427 CGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGCTTCAAGGCTGAGGAGGT 2486
QY 2223 GAATCGGCTTCAATGGAGCAGACGCTGCTTACGCTGTGTGAGGACCCGTCAGGGGCGAG 2282
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QY 2283 TGTCCCTCGAATCTCGAGAACCTGTCTGGCTTCCCTCCCAAGGAGATGAGGATGG 2342
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QY 2343 TGCTCTGAGGAAACTATGTGCCGCTCCAGCTCCTCCAGTCCAACTGATGGGCCAGATG 2402
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QY 2403 CAGCAGGAGCCAGAGGACAGAGAGGATCTTTCCAAACCATCATCTGCTGCTGCTGGGG 2462
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QY 2463 TCCAGT 2469
Db 2727 TCCAGT 2733

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RESULT 2
US-11-013-090-4
; Sequence 4, Application US/11013090
; Publication No. US20050158827A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
; FILE OF INVENTION: RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
; FILE REFERENCE: MPI98-093P2RCP3DVIAM
; CURRENT APPLICATION NUMBER: US/11/013,090
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: US 09/439,165
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/421,134
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 09/258,633
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 60/114,078
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/108,322
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 4
; LENGTH: 2809
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (361)...(2652)
US-11-013-090-4

Query Match 99.7%; Score 2462.2; DB 24; Length 2809;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2464; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 63 TCTGTGCTGGACCGAGCAGCTCTCTCTCTAGGATGACCTCACCTCTCCAGCTCTCCAGT 122
Db 327 TCTGTGCTGGACCGAGCAGCTCTCTCTCTAGGATGACCTCACCTCTCCAGCTCTCCAGT 386
QY 123 TTTTCAGTTTGGAGACATTAGATGGAGGCCAAGAGATGGCTCTGAGCGGACAGAGGAAA 182
Db 387 TTTTCAGTTTGGAGACATTAGATGGAGGCCAAGAGATGGCTCTGAGCGGACAGAGGAAA 446
QY 183 GCTTGGATTTTGGAGCGGGCTGCCTCCATGGAGTCAAGTTCCAGGGCGAGAACCGGAA 242
Db 447 GCTTGGATTTTGGAGCGGGCTGCCTCCATGGAGTCAAGTTCCAGGGCGAGAACCGGAA 506
QY 243 ATTTCGCCCTCAGATTAAGAGTCAACCTCACTACCGAAGGAGAACAGGTGCCAGTACGC 302
Db 507 ATTTCGCCCTCAGATTAAGAGTCAACCTCACTACCGAAGGAGAACAGGTGCCAGTACGC 566
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Db 567 GGATCCAAACCGATTTTGGACCGAGATCGGCTCTTCAATGGGCTCTCCCGGGTGTCCCGGA 626
QY 363 GGATCTGGCTGGACTTCCAGAGTACCTTGAGCAAGACAGCAAGTACCTCACCGACTCGGA 422
Db 627 GGATCTGGCTGGACTTCCAGAGTACCTTGAGCAAGACAGCAAGTACCTCACCGACTCGGA 686
QY 423 ATACACAGAGGGCTCCACAGGTAAAGACGTGCTGATGAGGCTGTGCTGAACCTTAAGGA 482
Db 687 ATACACAGAGGGCTCCACAGGTAAAGACGTGCTGATGAGGCTGTGCTGAACCTTAAGGA 746
QY 483 CGAGTCAATGCTGCTGCACTTCTGCCATCTGCTGAGATCGACAGGACTCTGCGCAATCTCA 542
Db 747 CGAGTCAATGCTGCTGCACTTCTGCCATCTGCTGAGATCGACAGGACTCTGCGCAATCTCA 806
QY 543 GCCCTCTGGTAAATGCCCAAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCAAT 602
Db 807 GCCCTCTGGTAAATGCCCAAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCAAT 866
QY 603 CGCCATTTGAGAGAGAGAGTCTGAGTGTGTGAAAGCTCTCTGTTGAGAGATGGGGCAATGT 662
Db 867 CGCCATTTGAGAGAGAGAGTCTGAGTGTGTGAAAGCTCTCTGTTGAGAGATGGGGCAATGT 926
QY 663 GCATGCCCGGGCTCGGGCGCTTCTTCCAGAGGGCCCAAGGACTTGTCTTTTATTTTCGG 722
Db 927 GCATGCCCGGGCTCGGGCGCTTCTTCCAGAGGGCCCAAGGACTTGTCTTTTATTTTCGG 986
QY 723 TGAGTCACTCCCTCTCTTTTGGCCGCTTGCACCAAGCAGTGGGATGTGGTAAGCTACCTCT 782
Db 987 TGAGTCACTCCCTCTCTTTTGGCCGCTTGCACCAAGCAGTGGGATGTGGTAAGCTACCTCT 1046
QY 783 GGAAGAACCCACACAGCGCCCGCAGCTGAGGCCACTGACTCCAGGGGCAACACAGTCTCT 842
Db 1047 GGAAGAACCCACACAGCGCCCGCAGCTGAGGCCACTGACTCCAGGGGCAACACAGTCTCT 1106
QY 843 GCATGCCCTAGTATGATCTCGGACACTCAGCTGAGAACATTCGACTCTGGTACACAGCAT 902
Db 1107 GCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAACATTCGACTCTGGTACACAGCAT 1166

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QY 903 GTATGATGGGCTCCTCCAGCTGGGGCCGCCCTCTGCGCTACCGTGCAGCTTGAGACAT 962  
Db 1167 GTATGATGGGCTCCTCCAGCTGGGGCCGCCCTCTGCGCTACCGTGCAGCTTGAGACAT 1226  
QY 963 CGCAACCTGCGAGATCTCACGCTCTGAAGCTGGCCGCCAAGGAGGCAAGATCCAGAT 1022  
Db 1227 CGCAACCTGCGAGATCTCACGCTCTGAAGCTGGCCGCCAAGGAGGCAAGATCCAGAT 1286  
QY 1023 TTTTCAGGCACATCCTGCGAGCGGAGTTTTCAGGACTGAGCCACTTTTCCCGAAAGTTTAC 1082  
Db 1287 TTTTCAGGCACATCCTGCGAGCGGAGTTTTCAGGACTGAGCCACTTTTCCCGAAAGTTTAC 1346  
QY 1083 CGAGTGGTGTATGGGCTGTCCGGGTGTCCGTGTGATGACCTGGCTTCTGTGACAGCTTG 1142  
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QY 1143 TGAGGAGAACTCAGTGTGTGAGATCAATGGCTTTTCAATGCAAGAGCCGCCACCGACACCG 1202  
Db 1407 TGAGGAGAACTCAGTGTGTGAGATCAATGGCTTTTCAATGCAAGAGCCGCCACCGACACCG 1466  
QY 1203 AATGTCGTGTTTTGGAGCCCTGAACAACTGCTGCGAGCGAAATGGGATCTGCTCATCCC 1262  
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QY 1263 CAAGTTCTTTTAAACTTCTGTGTAACTCTGATCTACATGTTTCACTTACCGCTGTGTC 1322  
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QY 1443 CGAGCTGTGTACTTCTGGGGGGCCACGTTGTTCACTGTGATCTCGTTTCATACAGACTA 1502  
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Db 1827 CTTGGCCATCGAGTGTGTACCTGCCCTCTGCTGTGTGTCTGCGCTGGTGGCTGGCTGAA 1886  
QY 1623 CTTGCTTTACTATACAGTGGCTTCCAGCACACAGGCATCTACAGTGTCTATGATCCAGAA 1682  
Db 1887 CTTGCTTTACTATACAGTGGCTTCCAGCACACAGGCATCTACAGTGTCTATGATCCAGAA 1946  
QY 1683 GGTTCATCTCGGGACCTGCTGGCTTCTTCTGATCTACTTGTCTTCTTCTTCTTCTGGCTT 1742  
Db 1947 GGTTCATCTCGGGACCTGCTGGCTTCTTCTGATCTACTTGTCTTCTTCTTCTTCTGGCTT 2006  
QY 1743 CGCTGTAGCCCTGTGTAGCTGTAGCCAGGAGGCTTGGCGCCCGAAGCTCCTACAGGCC 1802  
Db 2007 CGCTGTAGCCCTGTGTAGCTGTAGCCAGGAGGCTTGGCGCCCGAAGCTCCTACAGGCC 2066  
QY 1803 CAATGCCACAGAGTCACTGACGCCATGGAGGACAGGAGGCAACCGGGCCCA 1862  
Db 2067 CAATGCCACAGAGTCACTGACGCCATGGAGGACAGGAGGCAACCGGGCCCA 2126  
QY 1863 GTACAGGGGTATCTCGAAGCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGGCGA 1922  
Db 2127 GTACAGGGGTATCTCGAAGCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGGCGA 2186  
QY 1923 GCTGGCTTCCAGGAGCAGCTGCACTTCCCGCGCATGCTGCTGTGCTGTGGCCTA 1982  
Db 2187 GCTGGCTTCCAGGAGCAGCTGCACTTCCCGCGCATGCTGCTGTGCTGTGGCCTA 2246  
QY 1983 CGTGCTGCTCACCTACATCTGCTGTCTCAATGCTCATCGCCCTCATGAGCGAGCCGT 2042

Db 2247 CGTGTGCTCACCTACATCTGCTCTCAACATGCTCATCGCCCTCATGAGCGAGACCGT 2306  
QY 2043 CAACAGTGTGCGCACTGACAGCTGAGCATCTGGAAGCTGCAAGAACCATCTCTGTGCTT 2102  
Db 2307 CAACAGTGTGCGCACTGACAGCTGAGCATCTGGAAGCTGCAAGAACCATCTCTGTGCTT 2366  
QY 2103 GGAGATGGAGATGCTATTGCTGTCAGGAGAGCAGCGGGCAGGTTGATGCTGAC 2162  
Db 2367 GGAGATGGAGATGCTATTGCTGTCAGGAGAGCAGCGGGCAGGTTGATGCTGAC 2426  
QY 2163 CTTTGGCACTAAGCCAGATGGCAGCCCGATCAGCGCTGGTCTTCAGGGTGGAGAGT 2222  
Db 2427 CTTTGGCACTAAGCCAGATGGCAGCCCGATCAGCGCTGGTCTTCAGGGTGGAGAGT 2486  
QY 2223 GAACTGGGCTTCATGGAGCAGACGCTGCTACGCTGTGTGAGGACCCCTCAGGGGCGAG 2282  
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QY 2283 TGTCCCTCGAACTCTCGAGAACCTGTCTGCTGCTCCCTCCCAAGGAGGATCAGGATG 2342  
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QY 2343 TGCCTCTGAGGAAACTATGTGCTGCTCCAGTCCCTCCAGTCCAACTGATGGCCAGATG 2402  
Db 2607 TGCCTCTGAGGAAACTATGTGCTGCTCCAGTCCCTCCAGTCCAACTGATGGCCAGATG 2666  
QY 2403 CAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCAAACCAATCTGCTGGCTCTGGGG 2462  
Db 2667 CAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCAAACCAATCTGCTGGCTCTGGGG 2726  
QY 2463 TCCAGT 2469  
Db 2727 TCCAGT 2733

RESULT 3  
US-10-168-651-30  
; Sequence 30, Application US/10168651  
; Publication No. US20030171275A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: BURFORD, Neil  
; APPLICANT: AU-YOUNG, Janice  
; APPLICANT: LU, Dyung Aina M.  
; APPLICANT: YANG, Junming  
; APPLICANT: REDDY, Roopa  
; APPLICANT: LAL, Preeti  
; APPLICANT: HILLMAN, Jennifer L.  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: YUE, Henry  
; APPLICANT: NGUYEN, Danniell B.  
; APPLICANT: YAO, Monique G.  
; APPLICANT: GANDHI, Ameen R.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: KHAN, Farran A.  
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS  
; FILE REFERENCE: PI-0005 PCT  
; CURRENT APPLICATION NUMBER: US/10/168,651  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/172,000; 60/176,083; 60/177,332; 60/178,572; 60/179,758  
; 60/181,625  
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-21; 2000-01-28; 2000-02-02;  
; 2000-02-10  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PERL Program  
; SEQ ID NO 30  
; LENGTH: 2825  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature



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 Db 2418 GGAGATGGAGATGGCTATTGGTGGTGCAGGAAGACAGCGGCGAGGTGTGATGCTGAC 2477  
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 Db 2478 CGTTGGCACTAAGCCAGATGGCAGCCCGATGAGCCCTGGTGTTCAGGGTGGAGAGGT 2537  
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 Db 2778 TCCAGT 2784  
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RESULT 4

US-10-264-237-1401  
 ; Sequence 1401, Application US/10264237  
 ; Publication No. US20040009491A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Birse et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: P131P1  
 ; CURRENT APPLICATION NUMBER: US/10/264,237  
 ; CURRENT FILING DATE: 2002-10-04  
 ; PRIOR APPLICATION NUMBER: PCT/US01/16450  
 ; PRIOR FILING DATE: 2001-05-18  
 ; PRIOR APPLICATION NUMBER: US 60/205,515  
 ; PRIOR FILING DATE: 2000-05-19  
 ; NUMBER OF SEQ ID NOS: 2876  
 ; SOFTWARE: PatentIn Ver. 3.1  
 ; SEQ ID NO 1401  
 ; LENGTH: 2867  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
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 ; OTHER INFORMATION: n equals a,t,g, or c  
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 ; NAME/KEY: misc feature  
 ; LOCATION: (2845)..(2845)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (2850)..(2850)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
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 ; NAME/KEY: misc feature  
 ; LOCATION: (2858)..(2858)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
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 ; NAME/KEY: misc feature  
 ; LOCATION: (2866)..(2866)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; US-10-264-237-1401

Query Match 99.1%; Score 2447.4; DB 17; Length 2867;

Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2459; Conservative 3; Mismatches 4; Indels 1; Gaps 1;  
 QY 3 CGAGGCCGACGCGCAGCTGGGAGGAGACAGAGACCTTGCATCTCCATCTGCACAGAG 62  
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 Db 303 CAAACCCGACGCGCAGCTGGGAGGAGACAGGACCTTGCATCTCCATCTGCACAGAG 362  
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 QY 63 TCCTGGCTGGACCGAGCAGCTTCTCTCTCTAGGATGACCTCACCTTCAGCTCTCCAGT 122  
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 Db 363 TCCTGGCTGGACCGAGCAGCTTCTCTCTCTAGGATGACCTCACCTTCAGCTCTCCAGT 422  
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 QY 123 TTTTCAGTGGAGACATTAGATGGAGGCCAAGAATGGCTCTGAGGCGGACAGAGGAAA 182  
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 Db 423 TTTTCAGTGGAGACATTAGATGGAGGCCAAGAATGGCTCTGAGGCGGACAGAGGAAA 482  
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 QY 183 GCTGATTTTGGAGCGGGCTGCTCCCATGGAGTCAACAGTTCAGGGCGAGAGACCGGAA 242  
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 Db 483 GCTGATTTTGGAGCGGGCTGCTCCCATGGAGTCAACAGTTCAGGGCGAGAGACCGGAA 542  
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 Db 543 ATTGCGCCCTCAGATAAGAGTCAACCTCACTACGAAAGGGAACAGGTGCCAGTCAGCC 602  
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 Db 663 GGATCTGGCTGACTTCCAGAGTACCTGAGCAAGACCAAGTACCTCACCGACTCGGA 722  
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 QY 603 CGCCATTGAGAAAGAGAGTCTGAGTGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662  
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 QY 663 GCATGCCCGGGCTGCGGCGCTTCTTCCAGAAAGGCGCAAGGAGCTTGTCTTTTATTTTCGG 722  
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 QY 723 TGAGCTACCCCTCTCTTTTGGCCCTTGCACCAAGCAGTGGGATGTGGTAACTCTCTCTCT 782  
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 Db 1022 TGAGCTACCCCTCTCTTTGGCCCTTGCACCAAGCAGTGGGATGTGGTAACTCTCTCTCT 1081  
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 Db 1082 GGAGAACCCACACCGCCCGCCAGCTGAGGCGCACTGCTCCAGGGCAACACAGCTCTCT 1141  
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 QY 843 GCATGCCCTAGTGTGATGATCTCGGACAACTCAGCTGAGAAACATTTGCTGCTGCTGCTGCT 902  
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 Db 1142 GCATGCCCTAGTGTGATGATCTCGGACAACTCAGCTGAGAAACATTTGCTGCTGCTGCTGCT 1201  
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 QY 1023 TTTTCAGGACATCTCTGAGCGGGAGTTTTCAGGACTGAGCCACTTTTCCCGAAAGTTTTCAC 1082  
 |||||



QY	301	CCGGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCC	360	1381	AACTCCATGCTGCTGACGGGCCACATCCTTATCTCTGCTAGGGGGGATCTACCTCCTCGTG	1440
DB	587	CCGGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCC	646	1664	AACTCCATGCTGCTGACGGGCCACATCCTTATCTCTGCTAGGGGGGATCTACCTCCTCGTG	1723
QY	361	GAGGATCGGCTGGAATTCAGAGTACCTGAGCAAGCAGCAAGTACCTCACCGACTCG	420	1441	GGCCAGCTGTGTACTTCTGGCGGGCCACAGTGTTCATCTGGATCTCTGTTTCATAGACAGC	1500
DB	647	GAGGATCGGCTGGAATTCAGAGTACCTGAGCAAGCAGCAAGTACCTCACCGACTCG	706	1724	GGCCAGCTGTGTACTTCTGGCGGGCCACAGTGTTCATCTGGATCTCTGTTTCATAGACAGC	1783
QY	421	GAATACACAGAGGGCTCCACAGCTAAAGACGTGCTGATGAAGCTGTGCTGAACTTAAG	480	1501	TACTTTGAAATCCTCTTCTGTTTCAAGGCCCTGTCTACAGTGGTGTCCAGGTGCTGTGT	1560
DB	707	GAATACACAGAGGGCTCCACAGCTAAAGACGTGCTGATGAAGCTGTGCTGAACTTAAG	766	1784	TACTTTGAAATCCTCTTCTGTTTCCAGGCCCTGTCTACAGTGGTGTCCAGGTGCTGTGT	1843
QY	481	GACGGAGTCAATGCCCTGCAATTCGCCACTGTCTGCAGATCGACAGGACTCTGCGAATCCT	540	1561	TTCTCGGCCCATCAGGTGTGTACCTGCCCTGTGTTGTCTGCGCTGTGTGGCTGGCTG	1620
DB	767	GACGGAGTCAATGCCCTGCAATTCGCCACTGTCTGCAGATCGACAGGACTCTGCGAATCCT	826	1844	TTCTCGGCCCATCAGGTGTGTACCTGCCCTGTGTTGTCTGCGCTGTGTGGCTGGCTG	1903
QY	541	CAGCCCTGTGTAATGCCAGTGCACAGATGACTATTAACGAGGCCACAGCGCTCTGCGAC	600	1621	AACTGCTTTTACTATATACAGTGGCTTCCAGACACACAGGCATCTACAGTGTCTATGATCCAG	1680
DB	827	CAGCCCTGTGTAATGCCAGTGCACAGATGACTATTAACGAGGCCACAGCGCTCTGCGAC	886	1904	AACTGCTTTTACTATATACAGTGGCTTCCAGACACACAGGCATCTACAGTGTCTATGATCCAG	1963
QY	601	ATGCCAATTGAGAAGAGGAGTCTGCAAGTGTGAAAGCTCTCTGTTGAGAAATGGGGCAAT	660	1681	AAAGTCACTCCTCGGGACCTGTCTGGCTTCTTCTGTGATCTTCTTTTCGGC	1740
DB	887	ATGCCAATTGAGAAGAGGAGTCTGCAAGTGTGAAAGCTCTCTGTTGAGAAATGGGGCAAT	946	1964	AAAGTCACTCCTCGGGACCTGTCTGGCTTCTTCTGTGATCTTCTTTTCGGC	2023
QY	661	GTGCATGCCCGGCTGCGGCCGCTTCTTCCAGAGGGCCAAAGGACTTGTCTTTTATTC	720	1741	TTCTGCTGTAGCCCTGTGTAGCCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCTACAGGC	1800
DB	947	GTGCATGCCCGGCTGCGGCCGCTTCTTCCAGAGGGCCAAAGGACTTGTCTTTTATTC	1006	2024	TTCTGCTGTAGCCTGTGTAGCCTGTGAGCCAGGAGGCTTGGCGCCCGAAGCTCTACAGGC	2083
QY	721	GGTGAGTACCCCTCTCTTTGGCGGCTTGCACCAAGCAGTGGATGTGTAAGCTACCTC	780	1801	CCCAATGCCACAGAGTCACTGAGCCCATGAGGGGACAGAGGACAGAGGCCAACGGGGCC	1860
DB	1007	GGTGAGTACCCCTCTCTTTGGCGGCTTGCACCAAGCAGTGGATGTGTAAGCTACCTC	1066	2084	CCCAATGCCACAGAGTCACTGAGCCCATGAGGGGACAGAGGACAGAGGCCAACGGGGCC	2143
QY	781	CTGGAGAACCCACACAGCCCGCAGCTTCAGGCCCACTGACTCCACAGGGCAACACAGTC	840	1861	CAGTACAGGGGTATCTCTGGAAGCTCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGGC	1920
DB	1067	CTGGAGAACCCACACAGCCCGCAGCTTCAGGCCCACTGACTCCACAGGGCAACACAGTC	1126	2144	CAGTACAGGGGTATCTCTGGAAGCTCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGGC	2203
QY	841	CTGCATGCCCTAGTGATGATCTCGGACAACTCAGCTGAGAACATTTGACCTGTGTGACGAC	900	1921	GAGCTGGCCTTCCAGGAGCAGCTGCATTTCCGCGGCATGTGTCTGTCTGTCTGGCC	1980
DB	1127	CTGCATGCCCTAGTGATGATCTCGGACAACTCAGCTGAGAACATTTGACCTGTGTGACGAC	1186	2204	GAGCTGGCCTTCCAGGAGCAGCTGCATTTCCGCGGCATGTGTCTGTCTGTCTGGCC	2263
QY	901	ATGTATGATGGGCTCTCAGCTGCGGCGGCTCTGCCCTACCGTGACAGCTTGAGGAC	960	1981	TAGCTGCTGCTCACCTACATCTCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACC	2040
DB	1187	ATGTATGATGGGCTCTCAGCTGCGGCGGCTCTGCCCTACCGTGACAGCTTGAGGAC	1246	2264	TAGCTGCTGCTCACCTACATCTCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACC	2323
QY	961	ATCGCAACTGACAGATCTCAGCCCTCTGAAGCTGGCCCGCCAGAGGAGCAAGATCGAG	1020	2041	GTCAACAGTGTGCCCACTGACAGCTGGAGCATCTGGAAGCTGCAAGAACCATCTCTGTC	2100
DB	1247	ATCGCAACTGACAGATCTCAGCCCTCTGAAGCTGGCCCGCCAGAGGAGCAAGATCGAG	1306	2324	GTCAACAGTGTGCCCACTGACAGCTGGAGCATCTGGAAGCTGCAAGAACCATCTCTGTC	2383
QY	1021	ATTTTCAGGCACATCTGACGCGGAGTTTTCAGGACTGAGCCACCTTTTCCGAAAGTTTC	1080	2101	CTGGAGATGGAGAAATGGCTATTGGTGTGCAGGAAGACAGCGGCAGGTGTGATGCTG	2160
DB	1307	ATTTTCAGGCACATCTGACGCGGAGTTTTCAGGACTGAGCCACCTTTTCCGAAAGTTTC	1366	2384	CTGGAGATGGAGAAATGGCTATTGGTGTGCAGGAAGACAGCGGCAGGTGTGATGCTG	2443
QY	1081	ACCGAGTGTGCTATGGGCTGTCCGGTGTCTGATGATGACCTGGCTTCTGTGGACAGC	1140	2161	ACCGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGTGTCTTCAAGGTGGAGGAG	2220
DB	1367	ACCGAGTGTGCTATGGGCTGTCCGGTGTCTGATGATGACCTGGCTTCTGTGGACAGC	1426	2444	ACCGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGTGTCTTCAAGGTGGAGGAG	2503
QY	1141	TGTGAGGAGAACTCAGTGTGGAGATCATTTGCCCTTTTCAATTGCAAGAGCCCGCACACAC	1200	2221	GTGAACTGGGCTTTCATGGGAGCAGACGCTGCCCTACGCTGTGTGAGGACCCGTGAGGGGCA	2280
DB	1427	TGTGAGGAGAACTCAGTGTGGAGATCATTTGCCCTTTTCAATTGCAAGAGCCCGCACACAC	1486	2504	GTGAACTGGGCTTTCATGGGAGCAGACGCTGCCCTACGCTGTGTGAGGACCCGTGAGGGGCA	2563
QY	1201	CGAATGTGCTTTTGGAGCCCTGAAACAACTGCTGACGGCGAAATGGGATCTGCTCATC	1260	2281	GGTGTCCCTCGAATCTCGAGAACCTGTCTGGCTTCCCTCCCAAGGAGGATGAGGAT	2340
DB	1487	CGAATGTGCTTTTGGAGCCCTGAAACAACTGCTGACGGCGAAATGGGATCTGCTCATC	1546	2564	GGTGTCCCTCGAATCTCGAGAACCTGTCTGGCTTCCCTCCCAAGGAGGATGAGGAT	2623
QY	1261	CCCAAGTCTCTTAAATCTCTGTGTAATCTGATCTACATGTTTCATCTTCAACGCTGTT	1320	2341	GGTGTCCCTCGAAGAAATATGTGCCCGTCCAGCTCCTCCAGTCCAACTGATGGCCACAG	2400
DB	1547	CCCAAGTCTCTTAAATCTCTGTGTAATCTGATCTACATGTTTCATCTTCAACGCTGTT	1606	2624	GGTGTCCCTCGAGGAATATGTGTGCCCGTCCAGCTCCTCCAGTCCAACTGATGGCCACAG	2683
QY	1321	GCCTACCATCAGCTTACCTGAAAGACAGCGCCCGCTCACCCTGAAAGCGGAGTTTGA	1380	2401	TGACAGCAGAGGCGCAGAGGACAGAGCAGAGGATCTTTCCAAACCATCTGCTGGCTCTG	2460
DB	1607	GCCTACCATCAGCTTACCTGAAAGACAGCGCCCGCTCACCCTGAAAGCGGAGTTTGA	1663	2684	TGACAGCAGAGGCGCAGAGGACAGAGCAGAGGATCTTTTCCAAACCATCTGCTGGCTCTG	2743
				2461	GGTCCCCAGT	2469









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QY 979 CTACGCTCTGAAGCTGGCGCCGCAAGAGGCGCAAGATCGAGATTTTCAGGCACATCCCTG 1038
Db 901 CTACGCTCTGAAGCTGGCGCCGCAAGAGGCGCAAGATCGAGATTTTCAGGCACATCCCTG 960
QY 1039 CAGCGGAGTTTTCAGGACTGAGCCACTTTCCGAAAGTTTCACCGAGTGGTCTATGGG 1098
Db 961 CAGCGGAGTTTTCAGGACTGAGCCACTTTCCGAAAGTTTCACCGAGTGGTCTATGGG 1020
QY 1099 CTTGTCGGGTGTCGCTGTATGACCTGGCTTTCTGTGACAGCTGTGAGGAGAACTCAGTG 1158
Db 1021 CCTGTCGGGTGTCGCTGTATGACCTGGCTTTCTGTGACAGCTGTGAGGAGAACTCAGTG 1080
QY 1159 CTGAGATCATTTGCTTTTCAATGCAAGAGCCCGCACCGACCAAGTGGTCTTTTGGAG 1218
Db 1081 CTGAGATCATTTGCTTTTCAATGCAAGAGCCCGCACCGACCAAGTGGTCTTTTGGAG 1140
QY 1219 CCCCTGAACAACTGCTGCGAGCGCAATGGGATCTGCTCATCCCCCAAGTTCTTTAAAC 1278
Db 1141 CCCCTGAACAACTGCTGCGAGCGCAATGGGATCTGCTCATCCCCCAAGTTCTTTAAAC 1200
QY 1279 TTCCTGTGTAATCTGATCTACATGTTCAATCTTCAACGCTGTGGCTTACCATCAGCCTACC 1338
Db 1201 TTCCTGTGTAATCTGATCTACATGTTCAATCTTCAACGCTGTGGCTTACCATCAGCCTACC 1260
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Db 1261 CTGAAGACAGGCGGCCCTCACCTGAAAGCGGAGTTGGAACTCCATGCTGCTGACG 1320
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Db 1321 GGCACATCTTATCTGCTAGGCGGATCTACCTCTCTGCGGCCAGCTGTGTTACTTTC 1380
QY 1459 TGGCGGCGCCAGTGTTCATCTGGATCTCGTTTCATAGACAGCTACTTTGAAATCCTTTC 1518
Db 1381 TGGCGGCGCCAGTGTTCATCTGGATCTCGTTTCATAGACAGCTACTTTGAAATCCTTTC 1440
QY 1519 CTGTTCCAGGCCCTGCTCAGAGTGGTCCAGAGTCTGTGTTTCTTGGCCATCAGTGG 1578
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QY 1579 TACCTGCCCTCTGTTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1638
Db 1501 TACCTGCCCTCTGTTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1639 CGTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAGAAAGTTCATCTGCGGGAC 1698
Db 1561 CGTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAGAAAGTTCATCTGCGGGAC 1620
QY 1699 CTGCTGGCTTCTTCTGATCTACTTAGTCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1758
Db 1621 CTGCTGGCTTCTTCTGATCTACTTAGTCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1759 AGCCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCTACAGGCCCAATGCCACAGAGTCA 1818
Db 1681 AGCCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCTACAGGCCCAATGCCACAGAGTCA 1740
QY 1819 GTGAGGCCCATCGAGGGACAGGAGGACGAGGGCCAAAGGGCCCAAGTACAGGGGTATCCTG 1878
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QY 1879 GAAGCCTCTTGGAGCTTTCAAAATTCACATCGGCATGGGCGAGCTGGCCCTCCAGAG 1938
Db 1801 GAAGCCTCTTGGAGCTTTCAAAATTCACATCGGCATGGGCGAGCTGGCCCTCCAGAG 1860
QY 1939 CAGCTGCACTTCCGCGGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1998
Db 1861 CAGCTGCACTTCCGCGGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
QY 1999 ATCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAGAGCGTCAACAGTGTGCCACT 2058
Db 1921 ATCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAGAGCGTCAACAGTGTGCCACT 1980
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QY 2059 GACAGCTGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTTGAGATGGAGATGGC 2118
Db 1981 GACAGCTGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTTGAGATGGAGATGGC 2040
QY 2119 TATTTGTTGTGAGGAAGAGCAGCGGCGAGGTGTGATCTGACCCGTTGGCACTAAGCCA 2178
Db 2041 TATTTGTTGTGAGGAAGAGCAGCGGCGAGGTGTGATCTGACCCGTTGGCACTAAGCCA 2100
QY 2179 GATGGCAGCCCGATGAGCGCTGGTCTTTTCAGGGTGGAGAGGTGAATCTGGGCTTCAITGG 2238
Db 2101 GATGGCAGCCCGATGAGCGCTGGTCTTTTCAGGGTGGAGAGGTGAATCTGGGCTTCAITGG 2160
QY 2239 GAGCAGACGCTGCTACGCTGTGTAGGAGCCCGTCAAGGGCAGGTGTCTCTCGAACTCTC 2298
Db 2161 GAGCAGACGCTGCTACGCTGTGTAGGAGCCCGTCAAGGGCAGGTGTCTCTCGAACTCTC 2220
QY 2299 GAGAACCCTGCTGCTGCTTCCCTCCCAAGGAGGATGAGGATGGTCTCTGAGGAAAC 2358
Db 2221 GAGAACCCTGCTGCTGCTTCCCTCCCAAGGAGGATGAGGATGGTCTCTGAGGAAAC 2280
QY 2359 TATGTCCCGTCCAGCTCTCCAGTCCAACTGATGCCCCAGATGCAGCAGGAGGCCAGAG 2418
Db 2281 TATGTCCCGTCCAGCTCTCCAGTCCAACTGATGCCCCAGATGCAGCAGGAGGCCAGAG 2340
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Db 2341 GACAGACGAGAGATCTTTCCAAACCAATCTGCTGGCTCT 2380
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## RESULT 8

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; Sequence 67, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, G'n 1
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2292)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAD26363
; DATABASE ENTRY DATE: 1999-04-07
US-10-342-844-67
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Query Match 92.9%; Score 2293.4; DB 17; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 97 ATGACCTCACCTCCAGCTCTCCAGTTTTCAGGTTTGGAGACATTAGATGAGGCCAAGAA 156
Db 1 ATGACCTCACCTCCAGCTCTCCAGTTTTCAGGTTTGGAGACATTAGATGAGGCCAAGAA 60
QY 157 GATGGCTCTCAGCGCGGACAGAGGAAAGCTGGATTTTGGGAGCGGGTGTCTCCCATGAG 216
Db 61 GATGGCTCTCAGCGCGGACAGAGGAAAGCTGGATTTTGGGAGCGGGTGTCTCCCATGAG 120
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QY	217	TCACAGTTCCAGGGCGAGGACCGGAATTCGCCCTCAGATAAGAGTCAACCTCAACTAC	276	1297	TACATGTTTCATCTTCAACGCTGTTCCTACCATCAGCTTACCTGAAGAAGCGGCGGC	1356
Db	121	TCACAGTTCCAGGGCGAGGACCGGAATTCGCCCTCAGATAAGAGTCAACCTCAACTAC	180	1201	TCACATGTTTCATCTTCAACGCTGTTCCTACCATCAGCTTACCTGAAGAAGCGGCGGC	1260
QY	277	CGAAAGGGAACAGGTGCACGTCAAGCGGATCCAAACCGATTTCACCGAGATCGGCTTC	336	1357	CCTCACCTGAAAGCGAGGTTGGAATTCATGCTGCTGACCGGGCCACATCTTATCTTG	1416
Db	181	CGAAAGGGAACAGGTGCACGTCAAGCGGATCCAAACCGATTTCACCGAGATCGGCTTC	240	1261	CCTCACCTGAAAGCGAGGTTGGAATTCATGCTGCTGACCGGGCCACATCTTATCTTG	1320
QY	337	AATGCGGTCTCCCGGGGTGTCCTCGAGATCTGCTGGAATTCACAGTAGTACCTGAGCAAG	396	1417	CTAGGGGGATCTACTCTCTCGTGGGCGAGCTGTGGTATCTTCTGGGGGCGCACGTGTTG	1476
Db	241	AATGCGGTCTCCCGGGGTGTCCTCGAGATCTGCTGGAATTCACAGTAGTACCTGAGCAAG	300	1321	CTAGGGGGATCTACTCTCTCGTGGGCGAGCTGTGGTATCTTCTGGGGGCGCACGTGTTG	1380
QY	397	ACAGCAAGTACTCTACCGACTCGGGAATACAGAGGGCTCCACAGGTAAGAGTGGCTG	456	1477	ATCTGATCTCTCTCATAGACAGTACTTTGAAATCTCTTCTGTTCCAGGCCCTGCTC	1536
Db	301	ACCAGCAAGTACTCTACCGACTCGGGAATACAGAGGGCTCCACAGGTAAGAGTGGCTG	360	1381	ATCTGATCTCTCTCATAGACAGTACTTTGAAATCTCTTCTGTTCCAGGCCCTGCTC	1440
QY	457	ATGAAGCTGTGCTGAACCTTAAGGACGGAGTCAATGSCCTGCATTCCTGCCACTGCTGCAG	516	1537	ACAGTGGTCTCCAGAGTGTGTTTCTTGGCCATCGAGTGGTACCTGCCCCCTGCTTGTG	1596
Db	361	ATGAAGCTGTGCTGAACCTTAAGGACGGAGTCAATGSCCTGCATTCCTGCCACTGCTGCAG	420	1441	ACAGTGGTCTCCAGAGTGTGTTTCTTGGCCATCGAGTGGTACCTGCCCCCTGCTTGTG	1500
QY	517	ATCGACAGGACTCTTGGCAATCTCAGCCCCCTGTAATGCCAGTGCCACAGATGACTAT	576	1597	TCCTGGCTGGTCTGGGCTGGCTGAACTCTGCTTTACTATACAGTGGCTTCCAGACACA	1656
Db	421	ATCGACAGGACTCTTGGCAATCTCAGCCCCCTGTAATGCCAGTGCCACAGATGACTAT	480	1501	TCCTGGCTGGTCTGGGCTGGCTGAACTCTGCTTTACTATACAGTGGCTTCCAGACACA	1560
QY	577	TACGAGGCCACAGCGCTCTGCAATCGCCATTTGAGAGAGAGTCTGCAGTGTGTGAAG	636	1657	GGCATCTACAGTGTATGATCCAGAGGTCATCTGCGGGACCTGCTGGCTTCTTCTG	1716
Db	481	TACGAGGCCACAGCGCTCTGCAATCGCCATTTGAGAGAGAGTCTGCAGTGTGTGAAG	540	1561	GGCATCTACAGTGTATGATCCAGAGGTCATCTGCGGGACCTGCTGGCTTCTTCTG	1620
QY	637	CTCTGCTGAGAAATGGGGCAATGTGCATGCCGGGCTGCGGCTTCTTCCAGAAG	696	1717	ATCTACTTAGTCTTCTCTTTCGGCTTCGCTGTAGCCCTGAGCCTGAGCCAGGAGCT	1776
Db	541	CTCTGCTGAGAAATGGGGCAATGTGCATGCCGGGCTGCGGCTTCTTCCAGAAG	600	1621	ATCTACTTAGTCTTCTCTTTCGGCTTCGCTGTAGCCCTGAGCCTGAGCCAGGAGCT	1680
QY	697	GGCCAGGGACTTGTCTTTTATTTTGGTGAGTACCCCTCTCTTTTGGCGCTTGCAACAAG	756	1777	TGGCGCCCGAAGCTCTCTACAGCCCAATGCGCACAGAGTCACTGAGCCCATGAGGGA	1836
Db	601	GGCCAGGGACTTGTCTTTTATTTTGGTGAGTACCCCTCTCTTTTGGCGCTTGCAACAAG	660	1681	TGGCGCCCGAAGCTCTCTACAGCCCAATGCGCACAGAGTCACTGAGCCCATGAGGGA	1740
QY	757	CAGTGGATGTGTAGACTACTCTCGGAGAACCCACACAGCCCGCAGCTTGCAGGCC	816	1837	CAGGAGGACAGGGAAACGGGGCCAGATACAGGGTATCTCGAAGCCTCTTGGAGCTC	1896
Db	661	CAGTGGATGTGTAGACTACTCTCGGAGAACCCACACAGCCCGCAGCTTGCAGGCC	720	1741	CAGGAGGACAGGGAAACGGGGCCAGATACAGGGTATCTCGAAGCCTCTTGGAGCTC	1800
QY	817	ACTGACTCCAGGGCAACAGTCTCTGATGCCCTAGTGTATCTCGGACAACTCAGCT	876	1897	TTCAAATTCACCATCGGCATGGCGAGCTGGCTTTCACAGGACAGTGCATCTCCGCGC	1956
Db	721	ACTGACTCCAGGGCAACAGTCTCTGATGCCCTAGTGTATCTCGGACAACTCAGCT	780	1801	TTCAAATTCACCATCGGCATGGCGAGCTGGCTTTCACAGGACAGTGCATCTCCGCGC	1860
QY	877	GAGAACATTCGACTGTGACAGCATGTATGATGGGCTCTCCAAAGTGGGGCCCGCTC	936	1957	ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2016
Db	781	GAGAACATTCGACTGTGACAGCATGTATGATGGGCTCTCCAAAGTGGGGCCCGCTC	840	1861	ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1920
QY	937	TGCCCTACCGTGTGAGGACATCCGCAACCTGACAGATCTCAGCCCTCTGAGAGCTG	996	2017	CTCATCGCCCTCATGAGCGAGACCGTCAACAGTGTGCGCACTGACAGCTGGAGCATCTG	2076
Db	841	TGCCCTACCGTGTGAGGACATCCGCAACCTGACAGATCTCAGCCCTCTGAGAGCTG	900	1921	CTCATCGCCCTCATGAGCGAGACCGTCAACAGTGTGCGCACTGACAGCTGGAGCATCTG	1980
QY	997	GGCCCAAGGAGGCAAGATCGAGATTTTCAGGCACATCTGACGGGAGTTTTCAGGA	1056	2077	AAGCTGCAGAAAGCCATCTCTGCTCTGGAGATGGGAATGGCTATTGGTGGTCAGGAAG	2136
Db	901	GGCCCAAGGAGGCAAGATCGAGATTTTTCAGGCACATCTGACGGGAGTTTTCAGGA	960	1981	AAGCTGCAGAAAGCCATCTCTGCTCTGGAGATGGGAATGGCTATTGGTGGTCAGGAAG	2040
QY	1057	CTGAGCCACTTTCCCAAGATTCACCGAGTGTGCTATGGGCTGTCCGGGTGTGCGCTG	1116	2137	AAGACGGGCGAGGTGTGATGTCTGAGCTGGCACTAAGCCAGATGGGAGCCCGGATGAG	2196
Db	961	CTGAGCCACTTTCCCAAGATTCACCGAGTGTGCTATGGGCTGTCCGGGTGTGCGCTG	1020	2041	AAGACGGGCGAGGTGTGATGTCTGAGCTGGCACTAAGCCAGATGGGAGCCCGGATGAG	2100
QY	1117	TATGACTGGCTTCTGTGAGCAGCTGTGAGAGAGATCACTAGTGTGGAGATCATTTGCCTTT	1176	2197	CGCTGCTGCTTTCAGGGGTGAGGAGGTGAACTGGGCTTCAITGGAGCAGACGCTGCTACG	2256
Db	1021	TATGACTGGCTTCTGTGAGCAGCTGTGAGAGAGATCACTAGTGTGGAGATCATTTGCCTTT	1080	2101	CGCTGCTGCTTTCAGGGGTGAGGAGGTGAACTGGGCTTCAITGGAGCAGACGCTGCTACG	2160
QY	1177	CATTGCAAGAGCCCGACACCGAAATGCTGTTTTTGGAGCCCTGGAACAACCTGCTG	1236	2257	CTGCTGTGAGGACCCGTGAGGGCGAGGTGCTCCCTCGAACTCTCGAGAACCTGCTCTGGCT	2316
Db	1081	CATTGCAAGAGCCCGACACCGAAATGCTGTTTTTGGAGCCCTGGAACAACCTGCTG	1140	2161	CTGCTGTGAGGACCCGTGAGGGCGAGGTGCTCCCTCGAACTCTCGAGAACCTGCTCTGGCT	2220
QY	1237	CAGCGAAATGGATCTGCTCATCCCCAAGTCTTCTTAAACTTCTGTGTAATCTGATC	1296	2317	TCCCTTCCCAAGAGGATGAGATGCTGCTCTGAGGAAAACTATGCTGCCGCTCCAGCTC	2376
Db	1141	CAGCGAAATGGATCTGCTCATCCCCAAGTCTTCTTAAACTTCTGTGTAATCTGATC	1200	2221	TCCCTTCCCAAGAGGATGAGATGCTGCTCTGAGGAAAACTATGCTGCCGCTCCAGCTC	2280
				2377	CTCCAGTCCCACTGA	2391



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QY 1777 TGGCGCCCGAAGTCTCTACAGGCCCAATGCGACAGAGTCACTGCAAGCCCATGAGGGA 1836
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QY 1897 TTCAAATTCACCATCGGCATGGGCGAGCTGGCCCTTCAGGAGCAGCTGCACTTCCGCGGC 1956
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QY 1957 ATGGTGTGCTGTGCTGTGCTGGCTAGCTGTGCTGTACCTACATCTCTGTCTGTCTCAACATG 2016
Db 1861 ATGGTGTGCTGTGCTGTGCTGGCTAGCTGTGCTGTACCTACATCTCTGTCTGTCTCAACATG 1920
QY 2017 CTGATCGCCCTCATGAGCGAGACCGTCAACAGTGTGCGCACTGACAGCTGAGCATCTGG 2076
Db 1921 CTGATCGCCCTCATGAGCGAGACCGTCAACAGTGTGCGCACTGACAGCTGAGCATCTGG 1980
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; Sequence 69, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, G'n J
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; FILE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 69
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2292)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1995, 2000, 2118
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 667
; OTHER INFORMATION: xaa = Any Amino Acid
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAD41724
; DATABASE ENTRY DATE: 1999-07-01
US-10-342-844-69
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Query Match 91.7%; Score 2263.2; DB 17; Length 2295;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2274; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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QY 97 ATGACCTCACCTCCAGCTCTCCAGTTTTCAGTTTGGAGCGGGTGCCTCCCAAGAA 156
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QY 157 GATGGCTCTGAGCGGACAGAGAAAGCTGGATTTTGGAGCGGGTGCCTCCCAAGAA 216
Db 61 GATGGCTCTGAGCGGACAGAGAAAGCTGGATTTTGGAGCGGGTGCCTCCCAAGAA 120
QY 217 TCACAGTTCCAGGGGAGGACCGGAAATTCGGCCCTCAGATAGAGTCAACCTCAACTAC 276
Db 121 TCACAGTTCCAGGGGAGGACCGGAAATTCGGCCCTCAGATAGAGTCAACCTCAACTAC 180
QY 277 CGAAGGGAACAGGTGCCAGTCAGCGGATCCAAACCGGATTTGACCGAGATCGGCTCTTC 336
Db 181 CGAAGGGAACAGGTGCCAGTCAGCGGATCCAAACCGGATTTGACCGAGATCGGCTCTTC 240
QY 337 AATGCGGTCTCCCGGGGTGTCCCGAGGATCTGGCTGGACTTCCAGAGTACCTTGACAAAG 396
Db 241 AATGCTGTCTCCCGGGGTGTCCCGAGGATCTGGCTGGACTTCCAGAGTACCTTGACAAAG 300
QY 397 ACCAGCAATGACTCAACCGACTCGGAATACAGAGGGGCTCCACAGGTGAAGTGCCTG 456
Db 301 ACCAGCAATGACTCAACCGACTCGGAATACAGAGGGGCTCCACAGGTGAAGTGCCTG 360
QY 457 ATGAGGCTGTGCTGAACCTTAAGGACGGAGTCAATGCTGCTGATTTGCCACCTGCTGAG 516
Db 361 ATGAGGCTGTGCTGAACCTTAAGGACGGGGTCAATGCTGCTGATTTGCCACCTGCTGAG 420
QY 517 ATCGACAGGGGACTCTGGCAATCTCAGCCCTTGTTAAATGCCAGTGCAAGATGACTAT 576
Db 421 ATCGACCGGGAATCTGGCAATCTCAGCCCTTGTTAAATGCCAGTGCAAGATGACTAT 480
QY 577 TACCGAGGCCACAGCGCTCTGCACATCGCCATTTGAAGAGAGGATCTGCAAGTGTGAAG 636
Db 481 TACCGAGGCCACAGCGCTCTGCACATCGCCATTTGAAGAGAGGATCTGCAAGTGTGAAG 540
QY 637 CTCCTGGTGGAGAAATGGGGCCCAATGTGCATGCCCGGGCTGCGGGCGCTTCTTCCAGAAG 696
Db 541 CTCCTGGTGGAGAAATGGGGCCCAATGTGCATGCCCGGGCTGCGGGCGCTTCTTCCAGAAT 600
QY 697 GGCAGAGGACTTGTCTTTTATTTTCGGTGAAGTACCCCTCTCTTTTGGCCGCTTGCAACAAG 756
Db 601 GGCAGAGGACTTGTCTTTTATTTTGGTGAAGTACCCCTCTCTTTTGGCCGCTTGCAACAAG 660
QY 757 CAGTGGGATGTGTTAAGCTACTCTCTGGAGAAACCCACACAGCCCGCCGCTGCAAGGCC 816
Db 661 CAGTGGGATGTGTTAAGCTACTCTCTGGAGAAACCCACACAGCCCGCCGCTGCAAGGCC 720
QY 817 ACTGACTCCCGAGGCAACACAGTCTCTGCTGCTGATGATGATCTCGGACAACTCAGCT 876
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PRIOR APPLICATION NUMBER: 60/056,636		Matches 2365; Conservative 10; Mismatches 5; Indels 70; Gaps 4;	
PRIOR FILING DATE: 1997-08-22			
PRIOR APPLICATION NUMBER: 60/056,874			
PRIOR FILING DATE: 1997-08-22			
PRIOR APPLICATION NUMBER: 60/056,910			
PRIOR FILING DATE: 1997-08-22			
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PRIOR APPLICATION NUMBER: 60/056,631			
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PRIOR FILING DATE: 1997-08-22			
PRIOR APPLICATION NUMBER: 60/048,964			
PRIOR FILING DATE: 1997-06-06			
PRIOR APPLICATION NUMBER: 60/057,650			
PRIOR FILING DATE: 1997-09-05			
PRIOR APPLICATION NUMBER: 60/056,884			
PRIOR FILING DATE: 1997-08-22			
PRIOR APPLICATION NUMBER: 60/057,669			
PRIOR FILING DATE: 1997-09-05			
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Best Local Similarity	96.5%; Pred. No. 0;		

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Db	379	AGCCTCCCTCCCTAGGATGACCTCACCTCCAGCTCTCCAGTTTTCAGTTTGGAGACAT	438
QY	140	TAGATGGAGGCCAAGAAGATGGCTCTGAGGCGGACAGAGGAAAGCTGGATTTTGGAGCG	199
Db	439	TAGATGGAGGCCAAGAAGATGGCTCTGAGGCGGACAGAGGAAAGCTGGATTTTGGAGCG	498
QY	200	GGCTGCTCCCATGAGTCAAGTTCCAGGGGAGGACCGGAAATTCGCCCTTCAGATAA	259
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QY	260	GAGTCAACCTCAACTACCGAAAGGGAACAGGTCCAGTCAGCGGATCCAAACCCGATTG	319
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QY	320	ACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCGAGGATCTGGCTGGACTTC	379
Db	619	ACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCGAGGATCTGGCTGGACTTC	678
QY	380	CAGAGTACCTGAGCAAGACCAAGTACCTACCAGCTCGGAAATACACAGAGGGCTCCA	439
Db	679	CAGAGTACCTGAGCAAGACCAAGTACCTACCAGCTCGGAAATACACAGAGGGCTCCA	738
QY	440	CAGGTAAGACGTCCTGATGAAGGTGTGCTGAACCTTAAGGACCGAGTCAATGCTGCA	499
Db	739	CAGGTAAGACGTCCTGATGAAGGTGTGCTGAACCTTAAGGACCGAGTCAATGCTGCA	798
QY	500	TTCTGCCACTGTGCAGATTCGACAGGGACTCTGGCAATCTCAGCCCCCTGGTAAATGCC	559
Db	799	TTCTGCCACTGTGCAGATTCGACAGGGACTCTGGCAATCTCAGCCCCCTGGTAAATGCC	858
QY	560	AGTGACAGATGACTATTACGAGGCGACAGCGCTCTGCAATCGCCATTGAGAAGAGA	619
Db	859	AGTGACAGATGACTATTACGAGGCGACAGCGCTCTGCAATCGCCATTGAGAAGAGA	918
QY	620	GTCTGAGTGTGAGGCTCTGTTGGAGAAATGGGGCCAAATGTGATGCCGGCTGCG	679
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QY	680	GGCGCTTCTTCCAGAAAGGCCAAGGACTTGTCTTTTATTTTCGGTGAGCTACCCCTCTT	739
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QY	740	TGGCGCTTTCACCAAGCAGTGGGATGTGTAAGCTACCTCTTGGAGAACCCACACAGC	799
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QY	860	TCTCGGACAACTCAGCTGAGAAACATTGCACTGGTGACCAAGCATGTATGATGGGCTCCT	919
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QY	920	AGCTGGGGCCCGCTCTGCCCTACCGTGACGTTGAGGACATCCGCAACCTGCAGATC	979
Db	1217	AGCTGGGGCCCGCTCTGCCCTACCGTGACGTTGAGGACATCCGCAACCTGCAGATC	1276
QY	980	TCACGCTCTGAAGCTGGCGCCCAAGGAGGCAAGATCGAGATTTTCAGGCACATCCTGC	1039
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RESULT 14

US-09-809-391-314  
; Sequence 314, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002p2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 314  
; LENGTH: 2860  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (5)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (16)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-809-391-314

Query Match 83.5%; Score 2061.8; DB 10; Length 2860;  
Best Local Similarity 95.1%; Pred. No. 0;  
Matches 2364; Conservative 4; Mismatches 31; Indels 86; Gaps 20;

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Db 385 TCCTGGCTGGAAACCGAGCAGCTCTCTCTCTAGGATGACCTACCTCCAGCTCTCCAG 444  
QY 122 TTTTCAGTTGGAGACATAGATCGAGCCGAGAGAGTGTCTGAGCGGACAGAGAA 181  
Db 445 TTTTCAGTTGGAGACATAGATCGAGCCGAGAGAGTGTCTGAGCGGACAGAGAA 504  
QY 182 AGCTGGATTTTGGAGCGGCTGCTCCATGGAGTCAAGTTCCAGGCGGAGGACCGGA 241  
Db 505 AGCTGGATTTTGGAGCGGCTGCTCCATGGAGTCAAGTTCCAGGCGGAGGACCGGA 564  
QY 242 AATTGCGCCC-TCAGATAAGAGTCAACCT-CAACTACCGAAAGGAAACAGGTGCGAGTCA 299  
Db 565 AATTGCGCCCTTCAGATAAGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCGAGTCA 624  
QY 300 GCCGGATCCAAACCGATTGACCGAGATCGGCTCTTCAATCGGTCTCCCGGGGTGTC 359  
Db 625 GCCGGATCCAAACCGATTGACCGAGATCGGCTCTTCAATCGGTCTCCCGGGGTGTC 684  
QY 360 CGAGGATCTGGTGGACTTCCAGAGTACCTCAGCAAGACAGCAAGTACCTCAGCGACT- 418  
Db 685 CGAGGATCTGGTGGACTTCCAGAGTACCTCAGCAAGACAGCAAGTACCTCAGCGACTT 744  
QY 419 -CGGAATACACAGAGGCTCCACAGGTAAAGAGTGTCTGTAGTGAAGGCTGTCTG- AACCT 476  
Db 745 CGGAATACACAGAGGCTCCACAGGTAAAGAGTGTCTGTAGTGAAGGCTGTCTGAAACCT 803  
QY 477 TAAGACGAGAGTCAATGCTGTGATTTCTGCGCATCTGTCAGATCGACAGGACTCTGGCAA 536  
Db 804 TAAGACGAGGTCATGCTGTGATTTCTGCGCATCTGTCAGATCGACCGGACTCTGGCAA 863  
QY 537 TCCTCAGCCCTGGTAAATGCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCT 596  
Db |||||||

Db 864 TCCTCAGCCCTCGTAAATGCCAGTGCCAGATGACTATTACCGAGGCCACAGCGCTCT 923  
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Db |||||||

Db 924 GCACATCGCCATTTGAAAGAGAGTCTGAGTGTGAAGCTCTCTGGTGGAGAAATGGGG 983  
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QY 954 TGAGGACATCCGCAACTGCAGGATCTCAGGCTCTGAAAGCTGGCGCCCAAGGAGGCA 1013  
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QY 1254 GCTCATCCCCAAGTTCTTTAACTTCTTAACTTCTTAACTTCTTAACTTCTTAACTTCT 1313  
Db 1584 GCTCATCCCCAAGTTCTTTAACTTCTTAACTTCTTAACTTCTTAACTTCTTAACTTCT 1643  
QY 1314 CGCTGTGCTTACCATCAGCTTACCTTGAAGAGCAGCGCCCTCACTGAAAGCGGA 1373  
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QY 1374 GGTGGAAACTCCATGCTGCTGAGCGGCCACATCTTATCTGCTAGGGGGAATCTACCT 1433  
Db 1704 GGTGGAAACTCCATGCTGCTGAGCGGCCACATCTTATCTGCTAGGGGGAATCTACCT 1763  
QY 1434 CTTGCT-GGGCAGCTGTGTAATTCTGCGCGGCCACAGTGTTCATCTGGATCTCGTTCA 1492  
Db 1764 CTTGCTGGGCGCAGCTGTGTAATTCTGCGCGGCCACAGTGTTCATCTGGATCTCGTTCA 1823  
QY 1493 TAGACAGTACTTTT-GAAATCTCTTCTGTTTCCAGGCCCTGCG-TCACAGTGTGTGCCA 1550  
Db 1824 TAGACAGTACTTTTGGAAATCTCTTCTGTTTCCAGGCCCTGCTTTCACAGTGTGTGCCA 1883  
QY 1551 GGTGCTGTGTTTCTT-GGCCATCGAGTGTGTAATTCTGCGGCCCTGCTGTGTGTGCTGCTGTG 1608  
Db 1884 GGTGCTGTGTTTCTTGGGCCATCGAGTGTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1943  
QY 1609 CTGGGCTGGCTGAACCTGCTTTTACT-ATACTGTTGGC-TTCCAGCACACAGGCACTTACA 1666  
Db 1944 CTGGGCTGGCTGAACCTGCTTTTACTAATACTGTTGGGCTTTCAGCACACAGGC----- 1996

1667 GTGTATGATCCAGAAAGTCACTCCGCGGACCTGCTGGGCTTCTTCTGATCTACTTAG 1726  
 1997 -----AG 1998  
 1727 TCTTCTCTTTTGGCTTTCGCTGTAGCCCTGTGTAGCCTGAGCCAGGAGGCTTGGCGCCCG 1786  
 1999 TCTACAGTTTTCATGWTCCCTGAAGCCCTGTGTAGCCTGAGCCAGGAGGCTTGGCGCCCG 2058  
 1787 AGCTCTTACAGCCCCATGATCCACAGAGTCACTGAGCCCATGAGGAGGACAGGAGCG 1846  
 2059 AAGCTCTTACAGCCCCCAATGCCACAGAGTCACTGAGCCCATGAGGAGGACAGGAGCG 2118  
 1847 AGGCGAACGGGCCCCAGTACAGGGGTATCTGGAAGCTCTTGGAGCTTCAAAATTC 1906  
 2119 AGGCGAACGGGCCCCAGTACAGGGGTATCTGGAAGCTCTTGGAGCTTCAAAATTC 2178  
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 2147 CAGGTGTGATGTGACCGTTGGCACTAAG - CAGATGGCAGCCCGATGAGCGCTGGTGC 2205  
 2417 CAGGTGTGATGTGACCGTTGGCACTAAGCCAGATGGCAGCCCGATGAGCGCTGGTGC 2476  
 2206 TTCAAGGTGAGGAGGAGTGAATGGCTTCAAT - GGAAGCAGACGCTGCTACGCTGTGTGA 2264  
 2477 TTCAAGGTGAGGAGGAGTGAATGGCTTCAATGAGGAGCAGACGCTGCTACGCTGTGTGA 2536  
 2265 GGAAGCAGTCAAGGCGAGGTGCTGCTCGAACTCTCGAAACCTGTGCTGGCTTCCCTCC 2324  
 2537 GGAAGCAGTCAAGGCGAGGTGCTGCTCGAACTCTCGAAACCTGTGCTGGCTTCCCTCC 2596  
 2325 CAAGGAGGATGAGGATGGTCCCTCTGAGGAAACTATGTGCCCGTCCAGCTCTCCAGTC 2384  
 2597 CAAGGAGGATGAGGATGGTCCCTCTGAGGAAACTATGTGCCCGTCCAGCTCTCCAGTC 2656  
 2385 CAATGATGCCCCAGATGAGCAGGAGGCGCAGAGGACAGGACAGGATCTTTCCAAACCA 2444  
 2657 CAATGATGCCCCAGATGAGCAGGAGGCGCAGAGGACAGGACAGGATCTTTCCAAACCA 2716  
 2445 CATCTGCTGCTCTGGGGTCCCACT 2469  
 2717 CATCTGCTGCTCTGGGGTCCCACT 2741

RESULT 15  
 US-09-882-171-314  
 ; Sequence 314, Application US/09882171  
 ; Publication No. US20030175858A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: 186 Human Secreted proteins  
 ; FILE REFERENCE: P2002P2  
 ; CURRENT APPLICATION NUMBER: US/09/882,171  
 ; CURRENT FILING DATE: 2001-06-18  
 ; PRIOR APPLICATION NUMBER: 09/809,391  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 09/149,476  
 ; PRIOR FILING DATE: 1998-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US98/04493





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 5, 2005, 11:07:29 ; Search time 82 seconds

(without alignments)  
4771.079 Million cell updates/sec

Title: US-09-445-614B-2

Perfect score: 4004

Sequence: 1 MTSPPSSPVRLTLGGQE.....EEDGASENYPVQLQSN 764

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3945	98.5	764	2 Q9Y670	Q9Y670 homo sapien
3	3159	78.9	756	2 Q9WTR1	Q9WTR1 mus musculus
4	3158	78.9	756	2 Q6JGX2	Q6JGX2 f-11 rat/mo
5	3158	78.9	756	2 Q99K71	Q99K71 mus musculus
6	3051.5	76.2	761	2 Q9WUD2	Q9WUD2 rattus norv
7	3041.5	76.0	761	2 Q9QVH8	Q9QVH8 rattus norv
8	3028.5	75.6	762	2 Q9JMI8	Q9JMI8 rattus norv
9	1694	42.3	843	2 Q8QFN9	Q8QFN9 gallus gall
10	1652	41.3	838	2 Q35433	Q35433 rattus norv
11	1652	41.3	838	2 Q9JMS7	Q9JMS7 rattus norv
12	1651.5	41.2	839	2 Q9H304	Q9H304 homo sapien
13	1649	41.2	839	2 Q8K1W1	Q8K1W1 cavia porce
14	1649	41.2	840	2 Q69711	Q69711 canis famil
15	1648.5	41.2	839	2 Q9H0G9	Q9H0G9 homo sapien
16	1646	41.1	839	2 Q6RS3	Q6RS3 cavia porce
17	1645.5	41.1	839	2 Q6NER1	Q6NER1 homo sapien
18	1644.5	41.0	839	2 Q9W473	Q9W473 homo sapien
19	1642.5	41.0	839	2 Q704Y3	Q704Y3 mus musculus
20	1639.5	40.9	839	2 Q9NY22	Q9NY22 homo sapien
21	1638.5	40.9	842	2 Q6RX08	Q6RX08 oryctolagus
22	1617.5	40.4	829	2 Q68SW0	Q68SW0 mus musculus
23	1467	36.6	852	2 Q9DF63	Q9DF63 gallus gall
24	1467	36.6	853	2 Q6FY26	Q6FY26 homo sapien
25	1467	36.6	871	2 Q8NDV7	Q8NDV7 homo sapien
26	1467	36.6	871	2 Q6QC92	Q6QC92 homo sapien
27	1467	36.6	871	2 Q9HBC0	Q9HBC0 homo sapien
28	1465.5	36.6	871	2 Q9ER28	Q9ER28 rattus norv
29	1464	36.6	871	2 Q9HBA0	Q9HBA0 homo sapien
30	1458.5	36.4	871	2 Q9ES76	Q9ES76 mus musculus
31	1457.5	36.4	803	2 Q96RS7	Q96RS7 homo sapien

32	1457.5	36.4	871	2 Q9EPK8	Q9EPK8 mus musculus
33	1452.5	36.3	871	2 Q9BQZ4	Q9BQZ4 mus musculus
34	1447	36.1	803	2 Q91XR5	Q91XR5 mus musculus
35	1446.5	36.1	873	2 Q9ERZ7	Q9ERZ7 mus musculus
36	1442.5	36.0	778	2 Q9JM56	Q9JM56 rattus norv
37	1261	31.5	811	2 Q8NG64	Q8NG64 homo sapien
38	1153	28.8	790	2 Q8NDW7	Q8NDW7 homo sapien
39	1153	28.8	790	2 Q8NFH2	Q8NFH2 homo sapien
40	1146	28.6	791	2 Q8NET8	Q8NET8 homo sapien
41	1143	28.5	765	2 Q8NET9	Q8NET9 homo sapien
42	1139	28.4	791	2 Q8K424	Q8K424 mus musculus
43	1112.5	27.8	528	2 Q9Z182	Q9Z182 rattus norv
44	969	24.2	511	2 Q9H303	Q9H303 homo sapien
45	933	23.3	471	2 Q9JLM0	Q9JLM0 rattus norv

ALIGNMENTS

RESULT 1

Q9Y5S1 PRELIMINARY; PRT; 764 AA.  
AC Q9Y5S1;  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
DE Vanilloid receptor-like protein 1 (Transient receptor potential cation channel, subfamily V, member 2).  
DE channel, subfamily V, member 2).  
GN Name=VRL-1; Synonyms=TRPV2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99215558; PubMed=10201375; DOI=10.1038/18906;  
RA Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;  
RT "A capsaicin-receptor homologue with a high threshold for noxious heat";  
RL Nature 398:436-441(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22107054; PubMed=12077606; DOI=10.1038/nature00894;  
RA Smith G.D., Gunthorpe M.J., Kelsell R.E., Hayes P.D., Reilly P.,  
Racer P., Wright J.E., Jerman J.C., Walhin J.P., Ooi L., Egerton J.,  
Charles K.J., Smart D., Randall A.D., Anand P., Davis J.B.;  
RT "TRPV3 is a temperature-sensitive vanilloid receptor-like protein.";  
RL Nature 418:186-190(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Sapich S., Schenck M., Svejnar M., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Vallaloon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]



```
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A.
RP TISSUE=Skin;
RC Strausberg R.;
RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF129112; AD26363.1; -.
DR EMBL; AJ487963; CAD32310.1; -.
DR EMBL; BC018926; AAH18926.1; -.
DR EMBL; BC051305; AAH51305.1; -.
DR Genew; HGNC:18082; TRPV2.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005216; F:ion channel activity; TAS.
DR GO; GO:0015075; F:ion transporter activity; TAS.
DR GO; GO:0007600; P:sensory perception; TAS.
DR GO; GO:0006810; P:transport; TAS.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR Pfam; PF00023; Ank; 4.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR SMART; SM00248; ANK; 4.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 764 AA; 85980 MW; A73E3696E70F91E9 CRC64;

Query Match 100.0%; Score 4004; DB 2; Length 764;
Best Local Similarity 100.0%; Pred. No. 2.8e-275;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPSSSPVFRLETLDDGGQDGEADRGKLDGSGLPMPMESQFGEDRKFAPQIRVNLNY 60
DB 1 MTPSSSPVFRLETLDDGGQDGEADRGKLDGSGLPMPMESQFGEDRKFAPQIRVNLNY 60

QY 61 RKGTCASQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKYLTDSEYTGSTGKTCL 120
DB 61 RKGTCASQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKYLTDSEYTGSTGKTCL 120

QY 121 MKAVLNLDKGVNACILPLLIQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLOQVK 180
DB 121 MKAVLNLDKGVNACILPLLIQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLOQVK 180

QY 181 LLVENGANVHARACGRFFQKGQCTCFYFGBELPLSLAACTKQWDVSVYLLNPHQPASLOA 240
DB 181 LLVENGANVHARACGRFFQKGQCTCFYFGBELPLSLAACTKQWDVSVYLLNPHQPASLOA 240

QY 241 TDSQGNVTNLHALVMSDNSAENIALVTSMDGLLQAGARLCPTVQLEDIRNLQDLTFLKL 300
DB 241 TDSQGNVTNLHALVMSDNSAENIALVTSMDGLLQAGARLCPTVQLEDIRNLQDLTFLKL 300

QY 301 AAEKGKTEIFRHILQREFSGLSHLRKFTWCYCPVRVSLYDLASVDSCEENSVLEIIAF 360
DB 301 AAEKGKTEIFRHILQREFSGLSHLRKFTWCYCPVRVSLYDLASVDSCEENSVLEIIAF 360

QY 361 HCKSPHRRMVVLEPLNKLQAKWDLII PKFFLNFLCNLIYMFIFTAVAHQPTLKKQAA 420
DB 361 HCKSPHRRMVVLEPLNKLQAKWDLII PKFFLNFLCNLIYMFIFTAVAHQPTLKKQAA 420

QY 421 PHLKAEGVNSMLLTGHTLILLLGGIYLLVQGLWYFWRHVPFIWTSFIDSYPEIILFQALL 480
DB 421 PHLKAEGVNSMLLTGHTLILLLGGIYLLVQGLWYFWRHVPFIWTSFIDSYPEIILFQALL 480

QY 481 TVVSQVLCFLAEWYLPPLVLSALVGLWNLIIYYTRGFQHTGIYSVMIQKVLRLDLRLFL 540
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Db 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRGRHSALHIAIEKRSIQCCKV 180  
 Qy 181 LLVENGANVHARACGRFFQKQGTCTFYFGEPLPLSLAACTKQWDVSYLLENPHOPASLOA 240  
 Db 181 LLVENGANVHARACGRFFQKQGTCTFYFGEPLPLSLAACTKQWDVSYLLENPHOPASLOA 240  
 Qy 241 TDSQGNVTLHALVMI SDNSAENALTVMYDGLQAGARLCPTVQLEDIRNLQDLTPLKL 300  
 Db 241 TDSQGNVTLHALVMI SDNSAENALTVMYDGLQAGARLCPTVQLEDIRNLQDLTPLKL 300  
 Qy 301 AAKEGKIEIFRHILOREFSGLSLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360  
 Db 301 AAKEGKIEIFRHILOREFSGLSLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360  
 Qy 361 HCKSPHRHVMVLEPLNKLQAKWDLILPKFFLNFCLNIYMFIFTAVAYHQTLLKQAA 420  
 Db 361 HCKSPHRHVMVLEPLNKLQAKWDLILPKFFLNFCLNIYMFIFTAVAYHQTLLKQAA 420  
 Qy 421 PHLKAEGVNSMLTGHILILGGLYLLVGLQWYFWRHVFIFWISFIDSYPEILFLFOALL 480  
 Db 421 PHLKAEGVNSMLTGHILILGGLYLLVGLQWYFWRHVFIFWISFIDSYPEILFLFOALL 480  
 Qy 481 TVVSVQLCFIAIEWYLPVLLVLSALVGLWNLNLLYTRGFQHTGIYSVMIQKVIKDLRLFL 540  
 Db 481 TVVSVQLCFIAIEWYLPVLLVLSALVGLWNLNLLYTRGFQHTGIYSVMIQKVIKDLRLFL 540  
 Qy 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQYRGILEASLEL 600  
 Db 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQYRGILEASLEL 600  
 Qy 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
 Db 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
 Qy 661 KLOKAI SVLEMENGYWCRKQKQAGVMLTVGTGPDGSDPDRWCFRVEEVNWSAQEOTLPT 720  
 Db 661 KLOKAI SVLEMENGYWCRKQKQAGVMLTVGTGPDGSDPDRWCFRVEEVNWSAQEOTLPT 720  
 Qy 721 LCBDPSGAGVPTLENVPLASPKEDBDGASEENYVPVQLQSN 764  
 Db 721 LCBDPSGAGVPTLENVPLASPKEDBDGASEENYVPVQLQSN 764

## RESULT 3

Q9WTR1 ID Q9WTR1 PRELIMINARY; PRT; 756 AA.  
 AC Q9WTR1;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Growth factor regulated calcium channel.  
 GN Name=Trpv2; Synonyms=GRC;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57 Black-6; TISSUE=Spleen;  
 RX MEDLINE=20032759; PubMed=10559903; DOI=10.1038/11086;  
 RA Kanzaki M., Zhang Y.-Q., Mashima H., Li L., Shibata H., Kojima I.;  
 RT "Translocation of a calcium-permeable cation channel induced by  
 RT insulin-like growth factor-I.";  
 RL Nat. Cell Biol. 1:165-170(1999).  
 DR EMBL; AB021665; BAA78478.1; --  
 DR MGD; MGI:1341836; Trpv2.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR GO; GO:0005886; C:plasma membrane; IDA.  
 DR GO; GO:0005261; F:cation channel activity; IDA.  
 DR GO; GO:0009266; P:response to temperature; IDA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat\_channel\_TrpL.  
 DR InterPro; IPR005821; Ion\_trans.

DR InterPro; IPR004729; TRPChannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR Pfam; PF00023; Ank; 4.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR PRINTS; PRO1415; ANKTRIN.  
 DR PRINTS; PRO1768; TRPVRECEPTOR.  
 DR SMART; SM00248; ANK; 4.  
 DR TIGRFAMs; TIGR00870; tip; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT; 1.  
 DR ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.  
 KW SEQUENCE 756 AA; 85964 MW; 4C037D0F6066EF4C CRC64;

Query Match 78.9%; Score 3159; DB 2; Length 756;

Best Local Similarity 80.3%; Pred. No. 2.4e-215;

Matches 615; Conservative 55; Mismatches 84; Indels 12; Gaps 5;

Qy 1 MTSPTSSPVRLLETIDGGQDGEADRGKLDPGSLPPMESOFQGEDRFAQIRVNLNY 60

Db 1 MTSASNPFAFRLTSDGDEGSAEVNKGK----NEPPPMESPFQGEDRNFSPQIKVNLNY 56

Qy 61 RGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120

Db 57 RKLGPSQDPNRFDRDLFVSVRGVPEELTGLLEYLRTRTSKYLTDSEYTGSTGKTCL 116

Qy 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRGRHSALHIAIEKRSIQCCKV 180

Db 117 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDEFYRGRHSALHIAIEKRSIQCCKV 176

Qy 181 LLVENGANVHARACGRFFQKQGTCTFYFGEPLPLSLAACTKQWDVSYLLENPHOPASLOA 240

Db 177 LLVENGANVHARACGRFFQKQGTCTFYFGEPLPLSLAACTKQWDVSYLLENPHOPASLOA 236

Qy 241 TDSQGNVTLHALVMI SDNSAENALTVMYDGLQAGARLCPTVQLEDIRNLQDLTPLKL 300

Db 237 TDSQGNVTLHALVMI SDNSAENALTVMYDGLQAGARLCPTVQLEDIRNLQDLTPLKL 296

Qy 301 AAKEGKIEIFRHILOREFSGLSLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 359

Db 297 AAKEGKIEIFRHILOREFSGLSLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 356

Qy 360 FHCKSPHRHVMVLEPLNKLQAKWDLILPKFFLNFCLNIYMFIFTAVAYHQTLLKQAA 419

Db 357 FHCKSPHRHVMVLEPLNKLQAKWDLILPKFFLNFCLNIYMFIFTAVAYHQTLLKQAA 416

Qy 420 APHLKAEGVNSMLTGHILILGGLYLLVGLQWYFWRHVFIFWISFIDSYPEILFLFOAL 479

Db 417 IPSSKATFGDSMLLGHILILGGLYLLVGLQWYFWRHVFIFWISFIDSYPEILFLFOAL 476

Qy 480 LTWVSQVLCFLAIEWYLPVLLVLSALVGLWNLNLLYTRGFQHTGIYSVMIQKVIKDLRLFL 539

Db 477 LTWVSQVLCFLAIEWYLPVLLVLSALVGLWNLNLLYTRGFQHTGIYSVMIQKVIKDLRLFL 536

Qy 540 LIYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQYRGILEASLE 599

Db 537 LIYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQYRGILEASLE 594

Qy 600 LFKFTIGMELAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSI 659

Db 595 LFKFTIGMELAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSI 654

Qy 660 WKLOKAI SVLEMENGYWCRKQKQAGVMLTVGTGPDGSDPDRWCFRVEEVNWSAQEOTL 718

Db 655 WKLOKAI SVLEMENGYWCRKQKQAGVMLTVGTGPDGSDPDRWCFRVEEVNWSAQEOTL 714

Qy 719 PTLCEDPSGAGVPTLENVPLASPKEDBDGASEENYVPVQLQSN 764

Db 715 PTLCEDPSGAGVPTLENVPLASPKEDBDGASEENYVPVQLQSN 756

## RESULT 4

Q6JGX2 ID Q6JGX2 PRELIMINARY; PRT; 756 AA.

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AC O6JGX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TRPV2 protein.
OS F-11 rat/mouse fusion cell line.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
OC mouse/rat hybrid cell lines.
OX NCBI_TaxID=266798;
RN [1]
RP SEQUENCE FROM N.A.
RA Bender F., Mederos y Schnitzler M. V, Li Y., Ji A., Weihe E.,
RA Gudermann T., Schaefer M.K.H.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY487844; AAS66752.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR Pfam; PF00023; Ank; 3.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR SMART; SM00248; ANK; 4.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50098; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ SSSEQUENCE 756 AA; 85965 MW; C0E537AB2C96E1A8 CRC64;

Query Match 78.9%; Score 3158; DB 2; Length 756;
Best Local Similarity 80.3%; Pred. No. 2.9e-215;
Matches 615; Conservative 55; Mismatches 84; Indels 12; Gaps 5;

QY 1 MTSPPSPVRLFTLDGQDGSADRGKLDGSGLPMPESQPGEDRKFAQIRVNLNY 60
DB 1 MTSASNPAPARLTSDGDEGSAEVNKGK---NEPPMPESPPQGEDRNFSPQIKVNLNY 56
QY 61 RKTGASQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSTYEGSTGKTCL 120
DB 57 RKLGLSPQDPNRPDRDLFNVSVSRGVPPELTGLLEYLRRTSKYLTDSAYTEGSTGKTCL 116
QY 121 MKAVLMDQGNVACILPLQIDRDSGNPQPLVNAQCTDDYVRGHSALHIAIEKRSIQCVK 180
DB 117 MKAVLMDQGNVACILPLQIDRDSGNPQPLVNAQCTDEYVRGHSALHIAIEKRSIWCVK 176
QY 181 LLVENGANVHARACGRFFQKQGQCTCFYFGLPPLSLAACTKQMDVSVYLLNPHQPASLOA 240
DB 177 LLVENGANVHARACGRFFQKQGQCTCFYFGLPPLSLAACTKQMDVSVYLLNPHQPASLEA 236
QY 241 TDSQGVTLHALVMIISDENSEALVTSMYDGLLQAGARLCPVQLEDINQLDITPLKL 300
DB 237 TDSLGNVTLHALVMIADNSPENSALVTSMYDGLLQAGARLCPVQLEDICNHQGLTPLKL 296
QY 301 AAKEGKIEIPRHILQREFSGI-SHLGRKFTWCYGPVRVSLYDLASVDSCEENSVLIEITA 359
DB 297 AAKEGKIEIPRHILQREFSGLYQLSRKFTWCYGPVRVSLYDLSSVDSWEKNSVLIEITA 356
QY 360 FHCKSPHRRHVVLEPLNKLQAKWDLIIIPKPFINFLNLIYMFIFTAVAYHOPTLKQQA 419
DB 357 FHCKSPHRRHVVLEPLNKLQEKWDLIIPRFFNFACVLYVMIIFTIVAYHQPSLEQPA 416
QY 420 APLKRAVGNMMLTGHILILGGLIYLLVQWLYFWRRHVFIIWISIDSFFELFLFOAL 479
DB 417 IPSKATFGDSMLLGHILILGGLIYLLVQWLYFWRRHVFIIWISIDSFFELFLFOAL 476
QY 480 LTVVSVOLCFIAEWYLPILVSLVGLWNLNLYYTRGFQHTGIYSVMIOKVILRDLLREL 539
DB 479 LTVVSVOLCFIAEWYLPILVSLVGLWNLNLYYTRGFQHTGIYSVMIOKVILRDLLREL 536
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DB 477 LTVLSQVLRFEVETEWYLPVSSLVGLWNLNLYYTRGFQHTGIYSVMIOKVILRDLLREL 536
QY 540 LIYLVFLPGPAVALVSLSOEAWRPEAPTCGNATSVQPMGEQDEGNGAQYRGILEASLE 599
DB 537 LVYLVFLPGFAVALVSLSREARSKPAPDSNTTVEKPTLQGESE--PVPYGGILDASLE 594
QY 600 LFKFTIGMGLAFQELHFRGMVLLLLAYVLLTIVLLNMLIALMSETVNSVATDSWSI 659
DB 595 LFKFTIGMGLAFQELHFRGMVLLLLAYVLLTIVLLNMLIALMSETVNSVATDSWSI 654
QY 660 WKLOKAIISVLEMENGYWVCRKKQ-RAGVMLTVGTGKDGSPDERWCFRVEEVNNAWEOQL 718
DB 655 WKLOKAIISVLEMENGYWVCRKRHRAGRLLVGTGKDGIPDERWCFRVEEVNNAWAEKTL 714
QY 719 PTLCEDPGAGVPTLENPVLASPKPEDEGASEENYVPVQLQSN 764
DB 715 PTLSEDPGAGITGYKKNP-----SKPGKNSASEDHLPQLVQLQSH 756

RESULT 5
Q99K71
ID Q99K71 PRELIMINARY; PRT; 756 AA.
AC Q99K71;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE TRPV2 protein (Mus musculus 2 days neonate thymus thymic cells cDNA,
DE RIKEN full-length enriched library, clone:E430035F12 product:vanilloid
DE receptor-like protein 1, full insert sequence).
GN Name=Trpv2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Skolnick J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RT "High-efficiency full-length cDNA cloning.";
RN Meth. Enzymol. 303:19-44 (1999).
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Thymus;
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RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 [5]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=NOD; TISSUE=Thymus;  
 RC The FANTOM Consortium;  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 [6]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=NOD; TISSUE=Thymus;  
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 [7]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=NOD; TISSUE=Thymus;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikeguchi T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa K., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 [8]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=NOD; TISSUE=Thymus;  
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC005415; AA05415.1; -;  
 DR EMBL; AK089004; BAC40695.1; -;  
 DR MGD; MGI:1341836; Trpv2.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR GO; GO:0005886; C:plasma membrane; IDA.  
 DR GO; GO:0005261; P:cation channel activity; IDA.  
 DR GO; GO:0009286; P:response to temperature; IDA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat\_channel\_TrpL.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR004729; TrpChannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR Pfam; PF00023; Ank; 4.  
 DR Pfam; PF00520; Ion trans; 1.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR PRINTS; PR01768; TRPVRECEPTOR.  
 DR SMART; SM00248; ANK; 4.  
 DR TIGRPFAMs; TIGR00870; ttd; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;  
 KW Transport.  
 SQ SEQUENCE 756 AA; 85965 MW; C0E537AB3C86E1A8 CRC64;

Query Match 78.9%; Score 3158; DB 2; Length 756;  
 Best Local Similarity 80.3%; Pred. No. 2.9e-215;  
 Matches 615; Conservative 55; Mismatches 84; Indels 12; Gaps 5;  
 QY 1 MTPSSSPVFRLETLDCGQEDSGEADRGKLDGSGLPMPMESQFQGEDRKFPQIRVNLNY 60  
 DB 1 MTSASNPPAPRLTSDGDEGSAENVKKGK----NEPPPMESPFQGGDRNFSPQIKVNLNY 56  
 QY 61 RKGTCASQDPNRFDRDLRFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120  
 DB 57 RKGLGPSQDPNRFDRDLRFVSVRGVPBELTGLLEYLRTSKYLTSDSYTGSTGKTCL 116  
 QY 121 MKAVLNLDKGVNACILPLQLIDRDSGNPQPLVNAOCTDDYYRGHSAHIAIEKRSLOCVK 180  
 DB 117 MKAVLNLDKGVNACILPLQLIDRDSGNPQPLVNAOCTDFYRGHSAHIAIEKRSLSWCVK 176  
 QY 181 LLVENGANVHACACGFFQKQGTCTFYFGEPLSLAACTKQWDVSVLLENPHOPASLOA 240  
 DB 177 LLVENGANVHACACGFFQKQGTCTFYFGEPLSLAACTKQWDVSVLLENPHOPASLEA 236  
 QY 241 TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTFLKL 300  
 DB 237 TDSLGNVTLHALVMIADNSPENSALVIHMYDSLQMGARLCPTVQLEDICNHQGLTFLKL 296  
 QY 301 AAKEGKIEIFRHILQREFSGL-SHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIA 359  
 DB 297 AAKEGKIEIFRHILQREFSGLYQPLSRKFTWCYGPVRVSLYDLSSVDSWEKNSVLEIIA 356  
 QY 360 FHCKSPHRHMVLEPLNKLQAKWDLLIPKPLNPLNLIYMFITAVAYHQTPLKQOA 419  
 DB 357 FHCKSPHRHMVLEPLNKLQEKNDRLIPRFNFNFCYLVNMIIFTIVAYHQSLEQPA 416  
 QY 420 APHLKAEVGNMILTGHILLGGLYLLVQQLWYFWRHVPFIWISFIDSYFEILFLFOAL 479  
 DB 417 IPSSKATFGDSMLLGHILLGGLYLLVQQLWYFWRHVPFIWISFIDSYFEILFLVQAL 476  
 QY 480 LTVSVQVLCFLAIEWLYPLLVLSALVGLWNLNLYYTRGFQHTGTIYSVMIQVILRDLRLFL 539  
 DB 477 LTVSVQVLFVETEWYPLLVSVSLVGLWNLNLYYTRGFQHTGTIYSVMIQVILRDLRLFL 536  
 QY 540 LIYLVLPFGFVALVSLSQEAMRPBAPTGNATESVQPMGEQDEGNGAQYRGILEASLE 599  
 DB 537 LVYLVLPFGFVALVSLSREARSPKPEDSNITVTTEKPTLGQEE--PVPYGGILDSASLE 594  
 QY 600 LKFTTIGMGEIAPQEOELHFRGMVLLLLAYLVLLTYILLNMLIAMSSETVNSVATDSWSI 659  
 DB 595 LKFTTIGMGEIAPQEQRFQGVVLLLLAYLVLLTYILLNMLIAMSSETVNSVATDSWSI 654  
 QY 660 WKLQKAI SVLEMENGYWCKRKKO-RAGVMLTVGTPDGSPPDERWCPRVEENVNMAWSEQTLL 718  
 DB 655 WKLQKAI SVLEMENGYWCKRKRHRAGRLIKVGTGKDGIPDERWCPRVEENVNMAWSEKTL 714  
 QY 719 PTLCEPDPGAGVPTLENPVLASPPKDEDEGASEENVVLPQLQSN 764  
 DB 715 PTLSEDPGAGITGYKKNPT----SKPGKNSASEEDHLPLQVLOSH 756

## RESULT 6

Q9WUD2 ID Q9WUD2 PRELIMINARY; PRT; 761 AA.  
 AC Q9WUD2;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Vanilloid receptor-like protein 1.  
 GN Name=VRL-1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OK NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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RC STRAIN=Sprague-Dawley;
RX MEDLINE=99215558; PubMed=10201375; DOI=10.1038/18906;
RA Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;
RT "A capsaicin-receptor homologue with a high threshold for noxious
RL heat.";
RL Nature 398:436-441(1999).
DR EMBL: AF129113; AAD26364.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005261; F:cation channel activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0006812; P:cation transport; IEA.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat channel_TrpL.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR004729; TRPChannel.
DR InterPro: IPR008347; Vanil_receptor.
DR Pfam: PF00023; Ank; 4.
DR PRINTS: PR01415; ANKYRIN.
DR PRINTS: PR01768; TRPVRECEPTOR.
DR SMART: SM00248; ANK; 4.
DR TIGRFAMs: TIGR00870; trp; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW transport.
SQ SEQUENCE 761 AA; 86689 MW; 46A281183EB672F CRC64;

Query Match 76.2%; Score 3051.5; DB 2; Length 761;
Best Local Similarity 77.7%; Pred. No. 1e-207;
Matches 598; Conservative 62; Mismatches 93; Indels 17; Gaps 7;

Qy 1 MTSPPSSPVFRLETLDGQEGDEADRGKLDGSGGLPPMESQFGEDRKFAPQIRVNLNY 60
Db 1 MTSASSPPAFRLTSDGDEEGNAEVNKGQE----PPPMESPPQREDNRSSPQIKVNLNF 56

Qy 61 ----RKGTA-SQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKSYLTDSYETEGST 115
Db 57 IKRPKNKTSAPSQEQEPDRDRDLFVSVSRGVPEELTGLLEYLRWNSKYLTD SAYTEGST 116

Qy 116 GKTCLMKAVLNLDGYNACILPLLOIDRDSGNPQPLVNAOCTDDYYRGHSALHIAIEKRS 175
Db 117 GKTCLMKAVLNLDGYNACIMPLLOIDKDSGNPKPLVNAOCTDEFYQGHSAHIAIEKRS 176

Qy 176 LQCVKLLVNGANVHARACGRFFQKGQGTCTFFGELPLSLAACTKQWDVVSVLLENPHOP 235
Db 177 LQCVKLLVNGADVHLRACGRFFQKHQGTCTFFGELPLSLAACTKQWDVVSVLLENPHOP 236

Qy 236 ASLQATDSQNTVLHALVMSIDNSAENIALVTSMTDGLLQAGARLCTPTVQLSDIRNLQDL 295
Db 237 ASLEATDSLNTVLHALVMIADNSPENSALVIHMYDGLLQMGARLCTPTVQLSEISNHQGL 296

Qy 296 TPLKLAKEGKIIFRHILQREFSG-LSHLSRKFTTEWCYGPVRVSLYDLASVDSCBENS 354
Db 297 TPLKLAKEGKIIFRHILQREFSGPYQPLSRKFTTEWCYGPVRVSLYDLSSVDSEKNSV 356

Qy 355 LEIIAFHCKSPHRRMVVLEPLNKLQAKWDLIIPKFLLNCLNYMFTFVAVAHQPT 414
Db 357 LEIIAFHCKSPHRRMVVLEPLNKLQEKWDLVSRFFNFNFCYLVYMFITFVAVHQPS 416

Qy 415 LKQOAPHLKAEVGNMGLTGHTILLLGGIYLLVGLWYFWRHVFITWISFIDSYEILF 474
Db 417 LDQPAIPSSKATGESMLLGHILILLGGIYLLVGLWYFWRHVFITWISFIDSYEILF 476

Qy 475 LFQALLTVSVQVLCFLAIEWYLPVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVLIRD 534
Db 477 LQALLTVLSQVLRFMETEWYLPVLSVGLWNLNLYYTRGFQHTGIYSVMIQKVLIRD 536

Qy 535 LLRFLIYLVFLFGFAVALVSLSOEAWRPAPATGPNATESVQPMQEGDEGNAQVRGIL 594
Db 537 LLRFLIYLVFLFGFAVALVSLREARSAPRADNNSVTVEQPTVGQEEB--PAPYRSIL 594

Qy 595 EASLELFKFTIGMGELAFQQLFRGWVLLLLAYVLLTILLNMLIALMSETVNSVAT 654

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:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 595 DASLELFKFTIGMGELAFQQLFRGWVLLLLAYVLLTIVLLNMLIALMSETVNSVAT 654

Qy 655 DSWSIWKLQKAIISVLEMENGYWYC-RKKQACAGVMTVTGKPDGSDPDRWCFCRVEEVNWS 713
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 655 NSWSIWKLQKAIISVLEMENGYWYCRRKKHREGRLKVGTRGDTGTPDERWCPRVEEVNWA 714

Qy 714 WEQTLPITCEDSGAGVPTLENVPLASPPKDEDEGASENYPVQLLOS 763
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 715 WEKTLPTLSEDPSPGFTGNKNPT-----SKPGKNSASEEDHLPLQVLQS 760

RESULT 7
Q9QYH8 PRELIMINARY; PRT; 761 AA.
ID AC Q9QYH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stretch activated channel 2b.
GN Name=rsAC2b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishibashi K.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029330; BAA89637.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005261; F:cation channel activity; IEA.
DR GO: GO:0006812; P:cation transport; IEA.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat channel_TrpL.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR008347; Vanil_receptor.
DR Pfam: PF00023; Ank; 4.
DR PRINTS: PR01415; ANKYRIN.
DR PRINTS: PR01768; TRPVRECEPTOR.
DR SMART: SM00248; ANK; 4.
DR TIGRFAMs: TIGR00870; trp; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 761 AA; 86705 MW; 8977CDB1D5351EC8 CRC64;

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Query Match 76.0%; Score 3041.5; DB 2; Length 761;
Best Local Similarity 77.5%; Pred. No. 5.3e-207;
Matches 597; Conservative 62; Mismatches 94; Indels 17; Gaps 7;

Qy 1 MTSPPSSPVFRLETLDGQEGDEADRGKLDGSGGLPPMESQFGEDRKFAPQIRVNLNY 60
Db 1 MTSASSPPAFRLTSDGDEEGNAEVNKGQE----PPPMESPPQREDNRSSPQIKVNLNF 56

Qy 61 ----RKGTA-SQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKSYLTDSYETEGST 115
Db 57 IKRPKNKTSAPSQEQEPDRDRDLFVSVSRGVPEELTGLLEYLRWNSKYLTD SAYTEGST 116

Qy 116 GKTCLMKAVLNLDGYNACILPLLOIDRDSGNPQPLVNAOCTDDYYRGHSALHIAIEKRS 175
Db 117 GKTCLMKAVLNLDGYNACIMPLLOIDKDSGNPKPLVNAOCTDEFYQGHSAHIAIEKRS 176

Qy 176 LQCVKLLVNGANVHARACGRFFQKGQGTCTFFGELPLSLAACTKQWDVVSVLLENPHOP 235
Db 177 LQCVKLLVNGADVHLRACGRFFQKHQGTCTFFGELPLSLAACTKQWDVVSVLLENPHOP 236

Qy 236 ASLQATDSQNTVLHALVMSIDNSAENIALVTSMTDGLLQAGARLCTPTVQLSDIRNLQDL 295
Db 237 ASLEATDSLNTVLHALVMIADNSPENSALVIHMYDGLLQMGARLCTPTVQLSEISNHQGL 296

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QY 296 TPLKAAKEGKIEIFRHILQREFSG--LSHLSRKFTWCYGPVRVSLYDLASVDSCEANSV 354
DB 297 TPLKAAKEGKIEIFRHILQREFSGPYQPLSRKFTWCYGPVRVSLYDLSSVDSWEKNSV 356
QY 355 LEIIAFHCKSPHRRMVVLEPLNKLQAKWDLILPKFFLNFCLNLIYMFIFTAVAYHQT 414
DB 357 LEIIAFHCKSPHRRMVVLEPLNKLQAKWDLVSRFFNFACLYVMFIPTVVAHQPS 416
QY 415 LKQQAAPHLKAEVGNMMLTGHILLLGGIYLLVGLWYFWRHVPIMISPDYSFEILF 474
DB 417 LQOPALPSSKATPGESMMLLGHILLLGGIYLLVGLWYFWRHVPIMISFMDYSFEILF 476
QY 475 LFOALLTVVSVQVLCFLAIEMWYLLVLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRD 534
DB 477 LQOALLTVLSQVLRFMETEWYLLVLLVLSVGLWNLNLYYTRGFQHTGIYSVMIQVILRD 536
QY 535 LRLFLIYLVFLFGFAVALVLSQZAWRPEAPTGPNNATESVQPMQEGDEGNGAQYRGIL 594
DB 537 LRLFLIYLVFLFGFAVALVLSREARSPKAPEDNNSTVTQPTVQGBEE--PAPYRSIL 594
QY 595 EASLELPKFTIGMGLAFQELHFRGMVLLLLAYVLLTYLLLNLMIALMSETVNSVAT 654
DB 595 DASLELPKFTIGMGLAFQELHFRGMVLLLLAYVLLTYLLLNLMIALMSETVNSVAD 654
QY 655 DWSIWKLOKAI SVLEMENGYWMC--RKKORAGVMLTVGTPDGSPPDERCFCRVEEVNWA 713
DB 655 NWSIWKLOKAI SVLEMENGYWMCRRKKHREGRLKLVGTRGDGTPDERCFCRVEEVNWA 714
QY 714 WEQTLPTLCEDPGAGVPRTPLENPVLASPPKEDGASBENYVPVQL 763
DB 715 WEKTLPTLSEDPGPGITGNKNPT---SKPGKNSASBEDHLPLOVLOS 760

RESULT 8
Q9JM18 PRELIMINARY; PRT; 762 AA.
AC Q9JM18;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Ion channel.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RA Suzuki M.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB022332; BAA93435.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR Pfam; PF00023; Ank; 4.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR SMART; SM00248; ANK; 4.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS00088; ANK_REPEAT; 1.
DR PROSITE; PS02097; ANK_REPEAT_REGION; 1.
KM ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 762 AA; 86767 MW; C80970BC4195351E CRC64;

Query Match 75.6%; Score 3028.5; DB 2; Length 762;
Best Local Similarity 77.4%; Pred. No. 4.5e-206;
Matches 594; Conservative .62; Mismatches 94; Indels 17; Gaps 7;
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QY 1 MTSPPSSPVFRLETLTDGGQEDGSEADRGKLDGSGLPMPMESQFQGEDRKFAPIRVNLAY 60
DB 1 MTSASSPPAFRLTSDGDEGNAEVNKGQOE---PPMESPFQEDRNSSPQIKVNLNF 56
QY 61 ----RKGTGA--SQDPNPRFDRRLFNARSRGVPEDLAGLPEYLSKTSKYLTDSEYEGST 115
DB 57 IKRPKNTSAPSQSBPDRDLFSVVSRGVPBELTGLLEYLRWNSKYLTDASAYEGST 116
QY 116 GKTCLMKAVLNKCGVNACILPLLQIDRDSGNPQPLVNAQCTDDVYRGHSALHIAIEKRS 175
DB 117 GKTCLMKAVLNKCGVNACIMPELLQIDKDSGNPKLLVNAQCTDEFPYQHSALHIAIEKRS 176
QY 176 LQCVKLLVNGANVHARACGRFFQKGQCTCFYFGBELPLSLAACTQKQMDVSVYLLNPHOP 235
DB 177 LQCVKLLVNGADVHLRACGRFFQKHQCTCFYFGBELPLSLAACTQKQMDVSVYLLNPHOP 236
QY 236 ASLQATDSQGNVTLHALVMSDNSAENTALTVMYDGLLQAGARLCPTVOLEDIRNLQDL 295
DB 237 ASLEATDSLGNVTLHALVMIADNSPENSALVTHMYDGLLQMGARLCPTVQLEBEISNHQGL 296
QY 296 TPLKAAKEGKIEIFRHILQREFSG--LSHLSRKFTWCYGPVRVSLYDLASVDSCEANSV 354
DB 297 TPLKAAKEGKIEIFRHILQREFSGPYQPLSRKFTWCYGPVRVSLYDLSSVDSWEKNSV 356
QY 355 LEIIAFHCKSPHRRMVVLEPLNKLQAKWDLILPKFFLNFCLNLIYMFIFTAVAYHQT 414
DB 357 LEIIAFHCKSPHRRMVVLEPLNKLQAKWDLVSRFFNFACLYVMFIPTVVAHQPS 416
QY 415 LKQQAAPHLKAEVGNMMLTGHILLLGGIYLLVGLWYFWRHVPIMISFIDSFEILF 474
DB 417 LQOPALPSSKATPGESMMLLGHILLLGGIYLLVGLWYFWRHVPIMISFMDYSFEILF 476
QY 475 LFOALLTVVSVQVLCFLAIEMWYLLVLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRD 534
DB 477 LQOALLTVLSQVLRFMETEWYLLVLLVLSVGLWNLNLYYTRGFQHTGIYSVMIQVILRD 536
QY 535 LRLFLIYLVFLFGFAVALVLSQZAWRPEAPTGPNNATESVQPMQEGDEGNGAQYRGIL 594
DB 537 LRLFLIYLVFLFGFAVALVLSREARSPKAPEDNNSTVTQPTVQGBEE--PAPYRSIL 594
QY 595 EASLELPKFTIGMGLAFQELHFRGMVLLLLAYVLLTYLLLNLMIALMSETVNSVAT 654
DB 595 DASLELPKFTIGMGLAFQELHFRGMVLLLLAYVLLTYLLLNLMIALMSETVNSVAD 654
QY 655 DWSIWKLOKAI SVLEMENGYWMC--RKKORAGVMLTVGTPDGSPPDERCFCRVEEVNWA 713
DB 655 NWSIWKLOKAI SVLEMENGYWMCRRKKHREGRLKLVGTRGDGTPDERCFCRVEEVNWA 714
QY 714 WEQTLPTLCEDPGAGVPRTPLENPVLASPPKEDGASBENYVPVQL 760
DB 715 WEKTLPTLSEDPGPGITGNKNPT---SKPGKNSASBEDHLPLOV 757

RESULT 9
Q8QFN9 PRELIMINARY; PRT; 843 AA.
AC Q8QFN9;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Vanilloid receptor-like protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Dorsal root ganglia;
RX MEDLINE=21842900; PubMed=11853675; DOI=10.1016/S0092-8674(02)00637-2;
RA Jordt S.E., Julius D.;
RT "Molecular basis for species-specific sensitivity to 'hot' chili
```

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peppers.",
RL Cell 108:421-430(2002).
DR EMBL; AY072909; AAL78069.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004812; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_crans; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 4.
DR TIGRFAMs; TIGR00870; ttd; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR KEGG; K01100; ANK_REPEAT; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 843 AA; 96520 MW; ABB3592C9DC179C8 CRC64;

Query Match 42.3%; Score 1694; DB 2; Length 843;
Best Local Similarity 47.4%; Pred. No. 2.4e-111;
Matches 359; Conservative 118; Mismatches 217; Indels 64; Gaps 12;

Qy 4 PSSSFVFRLETLDDGQEDSGSEADRGKL---DFGSLGPPMESQFQEDRKFAPO-IRVNLN 59
Db |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
49 PSKSNIP-----ARRGRFVGMGCDKDMAPMDSFYQ-MDHLMAPSVLIKPHAN 93
Qy 60 YRKG-----TGASQDPNRFDRDLFNVAISRGVPPEDLAGLPEYLSKTYLTD 108
Db |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
94 MERGKLHKLLSTDITGCSKAFKPYDRRRIFDVARGSTKDLDDLLLYLNRTLLKHLTDD 153
Qy 109 EYTGSGTGKTCMLKAVLNLDGVNACILPLLQIDRDSGNPPLVNAOCTDDYVYRGHSAH 168
Db |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
154 EFKPEPTGKTCLLKAMLNLDGKNDTTPLLLDIAKKTGLKEFVNAEYTDNYKQTAH 213
Qy 169 IAEKRSQCVKLVANGANVHARACGRFFQGGQ-TCFYFGEIPLSLAACTKQWDVVSY 227
Db |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
214 IAIERRNNYLKVLAVQADVHARACGEFFEKIKGKPGFYFGEIPLSLAACTNOLCIVKF 273
Qy 228 LLENPHQASLQATDSQNTVYLHALVMI SDSNAENIALVTSMYDGLLOAGARLCPTVLE 287
Db |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
274 LLENPYQAADTAEDSMGMVHLITVEIADNTKNTKFTKYNINLLIGAKINPILKE 333
Qy 288 DIRNLQDITPLKAAEKGIKBIFRHILREFSG--LSHLSRKFTWCYGPVRVSLDYLAS 345
Db |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
334 ELTNKKGLTPLTAAKTGKIGIFAYILRRREIKDPECRHLSRKFTWAYGPVHSSLYDLS 393
Qy 346 VDSCEENSVEIIAIFHCKSPHRRMNVLEPLNKLLOAKWDLLIPK-PFLNFLCNLIYMF 404
Db |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
394 IDTCKNSVLEIIAYSSTPNRHEMLNRLLDQKDFVKHLYFYFNFVFAIHISI 453
Qy 405 FTAVAYHPTLKKQAAPH-LKAAVGNMMLTGHIILLGGLYLLVQGLWYFRRHVFHWI 463
Db |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
454 LTTAAYRYPVQKDKPPAFAGHSTGEYFRVTGEILSLVGLGIFFRGQIYFVQRPSLKT 513
Qy 464 SFIDSFYBILFQALLTVVSVQLCFIAIEWYLPLLVSALVGLWNLNLYYTRGFQHTGIY 523
Db |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
514 LIVDSYSVLFPVHSHLLLSLVLYFCQQLYVASWVPSALGAWNMLYYTRGFQOMGIY 573
Qy 524 SVMTKQVIRDLRLFLLLYLVFLFCFAVALYSLSQEAWRPEAPTGNATESVQPMEGGED 583
Db |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
574 SVMIAKMLRLDCRPMFVILVFLGFSFATVLLIED-----DNEGQDT 616
Qy 584 EGN-----GAQYRGILEASLELKFETIGMGEIAFOQLHFRGMVLLLLLAYVLL 632
Db |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
617 NSSEVARGSHYKRGRTS VNSLYYTCLEKFTIGMDLEFTEVRFKSVFVLLVLYVIL 676

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QY 90 DLGLPEYLSKSYLTDSYEGSTGKCLMKAVLNKDGYNACTLPLQLIDRDSGNPQ 149  
 DB 130 DLSLPLFLQSKKRTUTDFKDPETGKCLLKAMLNHNQNDTISLLDLARQNSLK 189  
 QY 150 PLVNAOCTDDYRGHSHALHIAIEKRSLQCVKLLVNGANVHARACGRPFQKQG-TCFYF 208  
 DB 190 EFNASYTDSYRGQTALHIAIERNNVLTLLVNGADVQAAANGDFPKTKGRPGFYF 249  
 QY 209 GELPLSLAACTQKQWVSVYLLNPHQPSAQATDSQGNVTVLHVMISONSABNTALVTS 268  
 DB 250 GELPLSLAACTQKQWVSVYLLNPHQPSAQATDSQGNVTVLHVMISONSABNTALVTS 309  
 QY 269 MYDGLLQAGARLCTVQLEDIRNLQDLTPLKAAKEGKIEIPHILOREF--SGLSHLGR 326  
 DB 310 MYNEILTLGAKYPTLKLBELTNKGTPLALAASSGKIGVLAIILOREIPPECHLGR 369  
 QY 327 KPTWCYGPVRSYLDLASVDSCEENSVEIIAF-HCKSPHRRHVMVLEPLNKLLOAKWD 385  
 DB 370 KFTWAYGPHVSSLYDLSCIDTCEKNSVLEVIAYSSETPNRHDMLLVEPLNKLLOAKWD 429  
 QY 386 LLIPK-FFNLFLCNLYMFIPTAVYHQPTLKKQAP--HLKAEVGNMMLTGHILILG 442  
 DB 430 RFVKRIFYNFYCLYMIIFTMAAYRPV---DGLPPYKMKNTVGDYFRVTGEILSVIG 486  
 QY 443 GIYLLVQOLWYFRRHVFVWISFDSYFEILPLFQALLTVVSVOLCFLEWVPLLVSA 502  
 DB 487 GFHFFRGIOYFLQRRPSVKTLFVDSYSELFFVQSLFLASVLYFSHRKEVACWVFS 546  
 QY 503 LVLGWNLNLYTTFGFOHTGYSYVMIQVILRDLLRFLLIYLVFLFQFAVALVSLSEAWR 562  
 DB 547 LALGWNMLYTTGFGQMGYIYVWIEKMIILRDLCPMFVYLVFLFGFSTAVVTLIED--- 603  
 QY 563 PEAPTEGNATESVQPMQEGDENGAQ-----YRGILEASLEIFKFTTIGMELAFQOLH 617  
 DB 604 -----GNESLSABPHRW---GPGCRSAKNSYSLSTCLELFTKFTIGMDLEFTENYD 655  
 QY 618 FRGWNLLIYVLLYVILLNMLIALMSETVNSVATDSWSIKLOKALISVLEWENGYYW 677  
 DB 656 FKAVFIILLAYVILTYILLNMLIALMGETVNSVATDSWSIKLOKALISVLEWENGYYW 715  
 QY 678 C-RKKORAGVMLTVGTPKDGSPDBRCFRVEEVNWSAQETLPTLCEDPGSA-GVPRITL 735  
 DB 716 CMKAFSGKLLQVGYTPDKDDYRCFRVDEVNWTWNTNNGIINEDPGNCEGVKRTLS 775  
 QY 736 NPVLASPPKEDDEGASEENVVYVOLLQ 762  
 DB 776 FSLRSQ---RVSGRNKNFALVPLLR 798

## RESULT 14

Q697L1 PRELIMINARY; PRT; 840 AA.  
 AC Q697L1  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Transient receptor potential V1.  
 GN Name=TRPV1;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Phelps P.T., Anches J.C., Correll C.C.;  
 RT "Cloning and Functional Characterization of Dog TRPV1."  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY568758; AAT71314.1;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005261; F:cation channel activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.

DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat channel\_TrpL.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR004729; TRPChannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion trans; 1.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR PRINTS; PR01768; TRPVRECEPTOR.  
 DR SMART; SM00248; ANK; 4.  
 DR TIGRFAMs; TIGR00870; trp; 1.  
 DR PROSITE; PS50088; ANK REPEAT; 1.  
 DR PROSITE; PS0297; ANK REP REGION; 1.  
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;  
 KW Transport.  
 SQ SEQUENCE 840 AA; 95236 MW; 5F5D5A366DC46459 CRC64;  
 Query Match 41.2%; Score 1649; DB 2; Length 840;  
 Best Local Similarity 50.0%; Pred. No. 3,7e-108;  
 Matches 340; Conservative 116; Mismatches 208; Indels 16; Gaps 9;  
 QY 64 TCASQDPNRPDRDRLENAVSRGVPEDLAGLPEYLSKSYLTDSYEGSTGKCLMKKA 123  
 DB 103 TAGSEKSLKYDRRKIFEAVQNCEELOSLLFLQSKKHLMDSEFKDPETGKTCLLKA 162  
 QY 124 VLNLKDGVNACILPLLIQIDRDSGNPQVLAQCTDDYRGHSHALHIAIEKRSLQCVKLLV 183  
 DB 163 MLNLHDGQNDTIPLLLEIARQDTSKLKELVNASYDTSYKQGTALHIAIERNNMALVTLV 222  
 QY 184 ENGANYHARACGRPFQKQG-TCFYFGEPLPLSLAACTQKQWVSVYLLNPHQPSAQATD 242  
 DB 223 ENGADVQAAANGDFPKTKGRPGFYFGEPLPLSLAACTQKQWVSVYLLNPHQPSAQATD 282  
 QY 243 SQGNVTVLHVMISONSABNTALVTSYDSEILFFVQSLFLASVLYFSHRKEVACWVFS 302  
 DB 283 SVGNTVHLVLEVAQNTADNTFVTSYNEILLGAKLHPTLKEGLTKKGLTPLALAA 342  
 QY 303 KEGKIEIPHILOREFS--GLSHLSRKFTWCYGPVRSYLDLASVDSCEENSVEIIAF 360  
 DB 343 RSGKIGVLAIILOREIQEPECHLSRKFTWAYGPHVSSLYDLSCIDTCEKNSVLEVIAY 402  
 QY 361 -HCKSPHRRHVMVLEPLNKLLOAKWDLIPK-FFNLFLCNLYMFIPTAVYHQPTLKKQ 418  
 DB 403 SSSETPNRHDMLLVEPLNKLLOAKWDRFVKRIFYNFYCLYMIIFTMAAYRPV--- 459  
 QY 419 AAP--HLKAEVGNMMLTGHILILGIGVLLVQGLVFWRRHVFVWISFDSYFEILFLF 476  
 DB 460 GLPPYKMKNTVGDYFRVTGEILSVLGGVYFFFGIOYFLQRRPSLTKLFDVSYSEMLFFV 519  
 QY 477 QALLTVVSVOLCFLEWVPLLVSAVLSQAWRPEAPTEGNATESVQPMQEGDENGAQVGRGLEA 536  
 DB 520 QSLFMLGTVVLYFCHHKEYVASVMSVFLANGWTNMLYTRGFGQMGYIYVWIEKMIILRDL 579  
 QY 537 RFLLIYLVFLFQFAVALVSLSQAWRPEAPTEGNATESVQPMQEGDENGAQVGRGLEA 596  
 DB 580 RFMFVYLVFLFGFSTAVVTLIEDGKNSVPT----ESTLHRWRGPGCRPPDSSNSLYST 635  
 QY 597 SLELFTKFTIGMELAFQOLHIFRGWVLLIYVLLNMLIALMSETVNSVATDS 656  
 DB 636 CLELFTKFTIGMGLFTENYDFKAVFIILLAYVILTYILLNMLIALMGETVNSVATDS 695  
 QY 657 WSLWKLOKALISVLEWENGYYW-C-RKKORAGVMLTVGTPKDGSPDBRCFRVEEVNWSAQE 715  
 DB 696 KNIWKLOKALISVLEWENGYYW-C-RKKORAGVMLTVGTPKDGSPDBRCFRVEEVNWSAQE 755  
 QY 716 QTLPTLCEDPGSA-GVPRITL 734  
 DB 756 TNVGIINEDPGNCEGVKRTL 775

## RESULT 15

Q9H0G9 PRELIMINARY; PRT; 839 AA.  
 ID Q9H0G9

AC Q9H0G9;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein DKFZp434K0220.  
 GN Name=DKFZp434K0220;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RG The German cDNA Consortium;  
 RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,  
 RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL136801; CAB66735.1; --  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005261; P:cation channel activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat channel\_TrpL.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR InterPro; IPR004729; TRPChannel.  
 DR InterPro; IPR008347; Vanil\_receptor.  
 DR InterPro; IPR008348; Vanil\_receptor2.  
 DR Pfam; PF00023; Ank; 3.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR PRINTS; PR01768; TRPVRECEPTOR.  
 DR PRINTS; PR01769; VRL2RECEPTOR.  
 DR SMART; SM00248; ANK; 4.  
 DR TIGRFAMs; TIGR00870; tip; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 KW ANK repeat; Hypothetical protein; Ion transport; Ionic channel;  
 KW Transmembrane; Transport.  
 SQ SEQUENCE 839 AA; 94949 MW; EA9BF7D603AE4760 CRC64;

Query Match 41.2%; Score 1648.5; DB 2; Length 839;  
 Best Local Similarity 48.5%; Pred. No. 4e-108;  
 Matches 344; Conservative 122; Mismatches 199; Indels 45; Gaps 11;

QY 74 FDRDLFNVAISGVPEDLAGLPEYLSKTYLTDSEYTGSTGKTCIMKAVLNKDGVNA 133  
 DB 113 YDRSIFEAVANNQCDLESLLFLQSKKHLTDNEFDPECTGKTLKAKMLNLDHGQNT 172

QY 134 CILPLIQIDRDSGNPQPLVNAOCTDDYYRGHSAIHIAIEKRSLOCVKLLVENGANVHARA 193  
 DB 173 TIPLLLEIARQTDLSKELVNASYTDYYKGQTAHIAIERNNMALVTLLVENGADYQAAA 232

QY 194 CGRFFFOKQOG-TCFYFGEPLSLAACTKQWDVVSYLLENPHOPASLOATDSOGNTVLHAL 252  
 DB 233 HGDFFFKTKRPGCFYFGEPLSLAACTNQLGIVKFLQNSQWQTADISARDSVGNVTVLHAL 292

QY 253 VMISDSNAENIALVTSMYDGLQAGARLCPTVQLEDIRNLQDITPLKAAKEGKIEIFRH 312  
 DB 293 VEADNTADNTKFTVSYNEIILGAKLHPTLKLLELTNKKGMTPLAALAAAGTKIGVLAY 352

QY 313 ILQREFS--GLSHLSRKFTWCYGPVRSIYDLASVDSCEANSVLEIIAF-HCKSPHRR 369  
 DB 353 ILQREIQEPCRHLSRKFTWAYGPHVSSLYDLSDICTCKNSVLEIAYSSSETPNRHD 412

QY 370 MVLLEPLNKLLOAKWDLIPK-FFLNPLCNLIYMFIFTAVAYHOPTLKKQAAPHLXAE-V 427  
 DB 413 MLIVPEPLNRLLOQKWRDFVVRIFVFLVCLYMLIFTMAAYRPV---DGLPPFQMEKI 469

QY 428 GNSMLTGHITLILGGIYLLVQGLWYFWRHVFIFWISFIDSYFEILFLQALLTVVSQVL 487  
 DB 470 GDYFRVTGEILSVLGGVYFFPRGIQYFLQRRPSMKTLFVDSYSEMLFFLQSLFMLATVVL 529

QY 488 CFLAIEWYLPPLVLSALVGLNLLYYTRGFQHTGIYSVMIQKVILRDLRFLLIYLVFLP 547

DB 530 YFSLHKEVVASVFSALGWTNMLYYTRGFQMGIIYAVMIKMLRDLCLRFMFVIVFLP 589  
 QY 548 GFAVALVSLSQEA-----WRPEAPTGNATESVQPMEGQDEGNGAQYRGIL 594  
 DB 590 GFSTAVVTLLIEDGKNDLSLPSESTSHRWGPACRPPDSS-----YNSLY 632  
 QY 595 EASLELPKFTIGMGELATQEQQLHPRGMVLLLLAYVLLTYILLNNMLIALMSETVNSVAT 654  
 DB 633 STCLELPKFTIGMGDLFTENYDFKAVFIILLAYVILTYILLNNMLIALMGETVNKIAQ 692  
 QY 655 DSMSIWKLQKATSVLEMENGYWMC-RKKQACGVMLTVGTPDGPSPDERWCPRVEEVNWAAS 713  
 DB 693 ESKNIWKQRAITIIDTEKSFUKMKRKAFRSKGLQVGYTPDGKDDYRCFRVDEVNWT 752

QY 714 WBOQTLPTLCEDPGSA-GVPRTLENPVLASPPKEDBEDGASEENYVPVQLIQ 762  
 DB 753 WNTNVGIINEDPGNCEGKVKRTLSFSLRSS-----RVSGRHWKNFALVPLLR 798

Search completed: October 5, 2005, 11:20:56  
 Job time : 86 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: / October 5, 2005, 11:23:55 ; Search time 167 Seconds  
(without alignments)

1899.094 Million cell updates/sec

Title: US-09-445-614B-2

Perfect score: 4004

Sequence: 1 MTSFSSPVRLTDLGGQE.....EDEDGASENYVPVQLQSN 764

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4004	100.0	764	9	US-09-828-466-4
2	4004	100.0	764	10	US-09-978-303-36
3	4004	100.0	764	14	US-10-000-823-6
4	4004	100.0	764	15	US-10-342-844-68
5	4004	100.0	764	16	US-10-757-262-26
6	4004	100.0	764	16	US-10-473-127-761
7	4004	100.0	764	16	US-10-473-127-762
8	4004	100.0	764	16	US-10-473-127-765
9	4004	100.0	764	16	US-10-473-127-770
10	4004	100.0	764	16	US-10-473-127-772
11	4004	100.0	764	16	US-10-473-127-776

12	4004	100.0	764	16	US-10-473-127-779	Sequence 779, App
13	4004	100.0	764	17	US-10-915-017-36	Sequence 36, Appl
14	4004	100.0	764	20	US-11-013-090-5	Sequence 5, Appl
15	3998	99.9	764	14	US-10-168-651-3	Sequence 3, Appl
16	3998	99.9	764	16	US-10-473-127-766	Sequence 766, App
17	3998	99.9	764	16	US-10-473-127-767	Sequence 767, App
18	3988.5	99.6	763	16	US-10-473-127-764	Sequence 764, App
19	3988.5	99.6	763	16	US-10-473-127-773	Sequence 773, App
20	3988.5	99.6	763	16	US-10-473-127-774	Sequence 774, App
21	3988.5	99.6	889	14	US-10-137-316-2	Sequence 2, Appl
22	3945	98.5	764	9	US-09-828-466-5	Sequence 5, Appl
23	3945	98.5	764	15	US-10-342-844-70	Sequence 70, Appl
24	3945	98.5	764	16	US-10-473-127-763	Sequence 763, App
25	3945	98.5	764	16	US-10-473-127-778	Sequence 778, App
26	3945	98.5	764	16	US-10-473-127-780	Sequence 780, App
27	3945	98.5	764	16	US-10-782-695-10	Sequence 10, Appl
28	3919	98.4	764	16	US-10-473-127-775	Sequence 775, App
29	3926	98.1	760	9	US-09-764-367A-9	Sequence 9, Appl
30	3375	84.3	644	15	US-10-342-844-44	Sequence 44, Appl
31	3258	81.4	630	16	US-10-473-127-777	Sequence 777, App
32	3258	81.4	630	20	US-11-013-090-20	Sequence 20, Appl
33	3159	78.9	756	15	US-10-342-844-86	Sequence 86, Appl
34	3158	78.9	756	15	US-10-342-844-52	Sequence 52, Appl
35	3051.5	76.2	761	10	US-09-978-303-4	Sequence 4, Appl
36	3051.5	76.2	761	15	US-10-342-844-46	Sequence 46, Appl
37	3051.5	76.2	761	17	US-10-915-017-4	Sequence 4, Appl
38	3041.5	76.0	761	15	US-10-342-844-34	Sequence 34, Appl
39	3036.5	75.8	727	10	US-09-978-303-23	Sequence 23, Appl
40	3036.5	75.8	727	16	US-10-473-127-769	Sequence 769, App
41	3036.5	75.8	727	16	US-10-473-127-771	Sequence 771, App
42	3036.5	75.8	727	17	US-10-915-017-23	Sequence 23, Appl
43	3028.5	75.6	762	15	US-10-342-844-98	Sequence 98, Appl
44	2789	69.7	665	14	US-10-027-828-18	Sequence 18, Appl
45	2669	66.7	511	15	US-10-264-237-2806	Sequence 2806, Ap

ALIGNMENTS

RESULT 1  
US-09-828-466-4  
; Sequence 4, Application US/09828466  
; Patent No. US2002035056A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Silos-Santiago, Immaculada  
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL  
; FILE REFERENCE: MNI-125CP  
; CURRENT APPLICATION NUMBER: US/09/828,466  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 09/544,797  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 764  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-828-466-4

Query Match	100.0%;	Score	4004;	DB	9;	Length	764;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	764;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MTSPSSPVRLTDLGGQDSEADRGKLDGSLPPMESQFQDGRKFAQIRVNLNY	60				
Db	1	MTSPSSPVRLTDLGGQDSEADRGKLDGSLPPMESQFQDGRKFAQIRVNLNY	60				
Qy	61	RKGTGASQDPNFRDRRLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYEGTGKTC	120				
Db	61	RKGTGASQDPNFRDRRLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYEGTGKTC	120				
Qy	121	MKAVLNLKDGVNACILFLQLIDRDSGNPQPLVNAQCTDDYYRGHSLHIAIEKRSLOCVK	180				

Db 121 MKAVLNKDGVNACILPLQLIDRDSGNPQPLVNAOCTDDYYRGHSALHIAIEKRSLOQVK 180  
QY 181 LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQMDVVSYLENPHQPASLOA 240  
Db 181 LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQMDVVSYLENPHQPASLOA 240  
QY 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVOLEDIRNLDLTPLKL 300  
Db 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVOLEDIRNLDLTPLKL 300  
QY 301 AAKEGKIEIFRHILOREFSGLSHL SRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF 360  
Db 301 AAKEGKIEIFRHILOREFSGLSHL SRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF 360  
QY 361 HCKSPHRHRMVVLEPLNKLQAKWDLII PKPFLNFCNLIIYMFIFTAVAYHQPTLKKQAA 420  
Db 361 HCKSPHRHRMVVLEPLNKLQAKWDLII PKPFLNFCNLIIYMFIFTAVAYHQPTLKKQAA 420  
QY 421 PHLKAEGVSNMLLTGHIILILGGIYLLVGQWLYFWRRHVFIWISFIDSYFEILFLFOALL 480  
Db 421 PHLKAEGVSNMLLTGHIILILGGIYLLVGQWLYFWRRHVFIWISFIDSYFEILFLFOALL 480  
QY 481 TVVSQVLCFLAEWYLLPLVLSALVGLWNLIIYYTRGFQHTGIYSVMIQKVILRDLRLFL 540  
Db 481 TVVSQVLCFLAEWYLLPLVLSALVGLWNLIIYYTRGFQHTGIYSVMIQKVILRDLRLFL 540  
QY 541 IYLVFLFGFAVALVSLSQEAWRPEA PTGNATESVQPMEGQDEGNGAQYRGILEASLEL 600  
Db 541 IYLVFLFGFAVALVSLSQEAWRPEA PTGNATESVQPMEGQDEGNGAQYRGILEASLEL 600  
QY 601 FKFTTGMGELAFQEQHFRGMVLLIILAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
Db 601 FKFTTGMGELAFQEQHFRGMVLLIILAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
QY 661 KLOKAI SVLEMENGYWCKKORAGVMLTVGTPKDGSPDERWCFCRVEEVNWNASWEOTLPT 720  
Db 661 KLOKAI SVLEMENGYWCKKORAGVMLTVGTPKDGSPDERWCFCRVEEVNWNASWEOTLPT 720  
QY 721 LCEDPSGAGVPRTLNPNVLASPPKEDGEGASENYPVQVLLQSN 764  
Db 721 LCEDPSGAGVPRTLNPNVLASPPKEDGEGASENYPVQVLLQSN 764

RESULT 2  
US-09-978-303-36  
; Sequence 36, Application US/09978303  
; Publication No. US20030049728A1  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: Nucleic acid sequences encoding  
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related  
; TITLE OF INVENTION: polypeptides and uses thereof  
; FILE REFERENCE: UCAL084CON  
; CURRENT APPLICATION NUMBER: US/09/978,303  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/235,451  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/072,151  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 08/915,461  
; PRIOR FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 764  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-978-303-36

Query Match 100.0%; Score 4004; DB 10; Length 764;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTPSSSSPVFRLETTLDGGQEDGSEADRGKLDPGSGLPMMESQFQGEDRKFAFOIRVNLNY 60  
Db 1 MTPSSSSPVFRLETTLDGGQEDGSEADRGKLDPGSGLPMMESQFQGEDRKFAFOIRVNLNY 60  
QY 61 RKGTGASQDDPNRFRDRDLFNAVSRGVDPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 120  
Db 61 RKGTGASQDDPNRFRDRDLFNAVSRGVDPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 120  
QY 121 MKAVLNKDGVNACILPLQLIDRDSGNPQPLVNAOCTDDYYRGHSALHIAIEKRSLOQVK 180  
Db 121 MKAVLNKDGVNACILPLQLIDRDSGNPQPLVNAOCTDDYYRGHSALHIAIEKRSLOQVK 180  
QY 181 LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQMDVVSYLENPHQPASLOA 240  
Db 181 LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQMDVVSYLENPHQPASLOA 240  
QY 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVOLEDIRNLDLTPLKL 300  
Db 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVOLEDIRNLDLTPLKL 300  
QY 301 AAKEGKIEIFRHILOREFSGLSHL SRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF 360  
Db 301 AAKEGKIEIFRHILOREFSGLSHL SRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF 360  
QY 361 HCKSPHRHRMVVLEPLNKLQAKWDLII PKPFLNFCNLIIYMFIFTAVAYHQPTLKKQAA 420  
Db 361 HCKSPHRHRMVVLEPLNKLQAKWDLII PKPFLNFCNLIIYMFIFTAVAYHQPTLKKQAA 420  
QY 421 PHLKAEGVSNMLLTGHIILILGGIYLLVGQWLYFWRRHVFIWISFIDSYFEILFLFOALL 480  
Db 421 PHLKAEGVSNMLLTGHIILILGGIYLLVGQWLYFWRRHVFIWISFIDSYFEILFLFOALL 480  
QY 481 TVVSQVLCFLAEWYLLPLVLSALVGLWNLIIYYTRGFQHTGIYSVMIQKVILRDLRLFL 540  
Db 481 TVVSQVLCFLAEWYLLPLVLSALVGLWNLIIYYTRGFQHTGIYSVMIQKVILRDLRLFL 540  
QY 541 IYLVFLFGFAVALVSLSQEAWRPEA PTGNATESVQPMEGQDEGNGAQYRGILEASLEL 600  
Db 541 IYLVFLFGFAVALVSLSQEAWRPEA PTGNATESVQPMEGQDEGNGAQYRGILEASLEL 600  
QY 601 FKFTTGMGELAFQEQHFRGMVLLIILAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
Db 601 FKFTTGMGELAFQEQHFRGMVLLIILAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
QY 661 KLOKAI SVLEMENGYWCKKORAGVMLTVGTPKDGSPDERWCFCRVEEVNWNASWEOTLPT 720  
Db 661 KLOKAI SVLEMENGYWCKKORAGVMLTVGTPKDGSPDERWCFCRVEEVNWNASWEOTLPT 720  
QY 721 LCEDPSGAGVPRTLNPNVLASPPKEDGEGASENYPVQVLLQSN 764  
Db 721 LCEDPSGAGVPRTLNPNVLASPPKEDGEGASENYPVQVLLQSN 764

RESULT 3  
US-10-000-823-6  
; Sequence 6, Application US/10000823  
; Publication No. US20030027164A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING A NC  
; TITLE OF INVENTION: HUMAN ION CHANNEL EXPRESSED IN SPINAL CORD AND BRAIN  
; FILE REFERENCE: D0109NP  
; CURRENT APPLICATION NUMBER: US/10/000,823  
; CURRENT FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 60/250,587  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 764

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-823-6

Query Match      100.0%; Score 4004; DB 14; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPSSPVFRLETLDDGGEDGSEADRGKLDGSGLPMPESQFQGEDRKFAPIQIRVNLNY 60
Db 1 MTSPSSPVFRLETLDDGGEDGSEADRGKLDGSGLPMPESQFQGEDRKFAPIQIRVNLNY 60

QY 61 RGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 120
Db 61 RGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 120

QY 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSIQCVK 180
Db 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSIQCVK 180

QY 181 LLVENGANVHARACGRFFQGGTCTFYFGEPLSLAACTKQWDVSVYLLENPHQASLOA 240
Db 181 LLVENGANVHARACGRFFQGGTCTFYFGEPLSLAACTKQWDVSVYLLENPHQASLOA 240

QY 241 TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLQAGARLCTVQLEDIRNLQDLTPLKL 300
Db 241 TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLQAGARLCTVQLEDIRNLQDLTPLKL 300

QY 301 AAKEGKIEIFRHIQREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIIF 360
Db 301 AAKEGKIEIFRHIQREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIIF 360

QY 361 HCKSPHRHVMVLEPLNKLQAKWDLIIKPFNLFLCNLIYMFIFTAVAYHPTLKKQAA 420
Db 361 HCKSPHRHVMVLEPLNKLQAKWDLIIKPFNLFLCNLIYMFIFTAVAYHPTLKKQAA 420

QY 421 PHLKAEVGNMMLTGHIILGIGIYLLVGQWYFWRHVFVWISFIDSIFYEILFLFOALL 480
Db 421 PHLKAEVGNMMLTGHIILGIGIYLLVGQWYFWRHVFVWISFIDSIFYEILFLFOALL 480

QY 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKVLRLDLRFL 540
Db 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKVLRLDLRFL 540

QY 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNPNATESVQPMQEGDEGNGAQYRGILEASLE 600
Db 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNPNATESVQPMQEGDEGNGAQYRGILEASLE 600

QY 601 FKFTIGMGLAFQEQHFRGMVLLLLAYVLLTYILLNNMLIAMSETVNSVATDSWSIW 660
Db 601 FKFTIGMGLAFQEQHFRGMVLLLLAYVLLTYILLNNMLIAMSETVNSVATDSWSIW 660

QY 661 KLQKAI SVLEMENGYWCRKQKQAGVMLTVGTGKPDGSPDERWCFRVEEVNWSWEOTLPT 720
Db 661 KLQKAI SVLEMENGYWCRKQKQAGVMLTVGTGKPDGSPDERWCFRVEEVNWSWEOTLPT 720

QY 721 LCEDPGAGVPRTLENPVLASPPKEDGASEENYVPVQLLQSN 764
Db 721 LCEDPGAGVPRTLENPVLASPPKEDGASEENYVPVQLLQSN 764
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## RESULT 4

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US-10-342-844-68
; Sequence 68, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, G'n I
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
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; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAD26363
; DATABASE ENTRY DATE: 1999-04-07
; US-10-342-844-68
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Query Match      100.0%; Score 4004; DB 15; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTSPSSPVFRLETLDDGGEDGSEADRGKLDGSGLPMPESQFQGEDRKFAPIQIRVNLNY 60

QY 61 RGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 120
Db 61 RGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 120

QY 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSIQCVK 180
Db 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSIQCVK 180

QY 181 LLVENGANVHARACGRFFQGGTCTFYFGEPLSLAACTKQWDVSVYLLENPHQASLOA 240
Db 181 LLVENGANVHARACGRFFQGGTCTFYFGEPLSLAACTKQWDVSVYLLENPHQASLOA 240

QY 241 TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLQAGARLCTVQLEDIRNLQDLTPLKL 300
Db 241 TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLQAGARLCTVQLEDIRNLQDLTPLKL 300

QY 301 AAKEGKIEIFRHIQREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIIF 360
Db 301 AAKEGKIEIFRHIQREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIIF 360

QY 361 HCKSPHRHVMVLEPLNKLQAKWDLIIKPFNLFLCNLIYMFIFTAVAYHPTLKKQAA 420
Db 361 HCKSPHRHVMVLEPLNKLQAKWDLIIKPFNLFLCNLIYMFIFTAVAYHPTLKKQAA 420

QY 421 PHLKAEVGNMMLTGHIILGIGIYLLVGQWYFWRHVFVWISFIDSIFYEILFLFOALL 480
Db 421 PHLKAEVGNMMLTGHIILGIGIYLLVGQWYFWRHVFVWISFIDSIFYEILFLFOALL 480

QY 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKVLRLDLRFL 540
Db 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKVLRLDLRFL 540

QY 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNPNATESVQPMQEGDEGNGAQYRGILEASLE 600
Db 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNPNATESVQPMQEGDEGNGAQYRGILEASLE 600

QY 601 FKFTIGMGLAFQEQHFRGMVLLLLAYVLLTYILLNNMLIAMSETVNSVATDSWSIW 660
Db 601 FKFTIGMGLAFQEQHFRGMVLLLLAYVLLTYILLNNMLIAMSETVNSVATDSWSIW 660

QY 661 KLQKAI SVLEMENGYWCRKQKQAGVMLTVGTGKPDGSPDERWCFRVEEVNWSWEOTLPT 720
Db 661 KLQKAI SVLEMENGYWCRKQKQAGVMLTVGTGKPDGSPDERWCFRVEEVNWSWEOTLPT 720

QY 721 LCEDPGAGVPRTLENPVLASPPKEDGASEENYVPVQLLQSN 764
Db 721 LCEDPGAGVPRTLENPVLASPPKEDGASEENYVPVQLLQSN 764
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```
RESULT 5
US-10-757-262-26
; Sequence 26, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Sillos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53017, 16852, 1587, 2207, 2245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MPI03-007PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-26

Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSSPVFRLETLDDGGQEDGSEADRGKLDGSGGLPPMESQFGEDRKFAQIRVNLNY 60
DB 1 MTSPPSSPVFRLETLDDGGQEDGSEADRGKLDGSGGLPPMESQFGEDRKFAQIRVNLNY 60
QY 61 RKG TGASQDPNRRDRDLFNAVSRGVDPDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
DB 61 RKG TGASQDPNRRDRDLFNAVSRGVDPDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRGRHSALHIAIEKRSIQCVK 180
DB 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRGRHSALHIAIEKRSIQCVK 180
QY 181 LIVENGANVHARACGFFQKGQCTCFYFGLPLSLAAC TKQWDVVSYLENPHOPASLOA 240
DB 181 LIVENGANVHARACGFFQKGQCTCFYFGLPLSLAAC TKQWDVVSYLENPHOPASLOA 240
QY 241 TDSQGNVTLHALVMISDNSAENIALVTSMDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300
DB 241 TDSQGNVTLHALVMISDNSAENIALVTSMDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300

Db 241 TDSQGNVTLHALVMISDNSAENIALVTSMDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300
QY 301 AAKEGKIEIFRHILQREFSGLSHLSRKETWCYGPVRVSLYDLASVDSCEENSVEIITAF 360
DB 301 AAKEGKIEIFRHILQREFSGLSHLSRKETWCYGPVRVSLYDLASVDSCEENSVEIITAF 360
QY 361 HCKSPHRHVMVLEBPLNKLQAKWDLILPKFFLNLCLNIYMFIFTAVAYHQTTLKQAA 420
DB 361 HCKSPHRHVMVLEBPLNKLQAKWDLILPKFFLNLCLNIYMFIFTAVAYHQTTLKQAA 420
QY 421 PHLKAEGVNSMLLTGHILLLGGIYLLVGQLMYFWRHVFVFIWISFIDSYFEILFLQALL 480
DB 421 PHLKAEGVNSMLLTGHILLLGGIYLLVGQLMYFWRHVFVFIWISFIDSYFEILFLQALL 480
QY 481 TVVSQVLCLAEIETWLPPLVLSALVGLNLLYYTRGFQHTGTYSMIQKVIIRDLLRELL 540
DB 481 TVVSQVLCLAEIETWLPPLVLSALVGLNLLYYTRGFQHTGTYSMIQKVIIRDLLRELL 540
QY 541 IYLVFLFGFAVALVSLSOEAWRPEAPTGP NATESVQPMEGQDEGNGAQYRGILEASLEL 600
DB 541 IYLVFLFGFAVALVSLSOEAWRPEAPTGP NATESVQPMEGQDEGNGAQYRGILEASLEL 600
QY 601 PKFTTGMGELAFQEQHLHFRGMVLLLLAYLLTYILLNMLIALMSETVNSVATDSWSIW 660
DB 601 PKFTTGMGELAFQEQHLHFRGMVLLLLAYLLTYILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAI SVLEMBNGYWCRCRKQORAGVMTVGTGKPGSDERWCPRVEEVNWSWEQTLP 720
DB 661 KLOKAI SVLEMBNGYWCRCRKQORAGVMTVGTGKPGSDERWCPRVEEVNWSWEQTLP 720
QY 721 LCEDPSGAGVPRTLNPNVLASPPKDEDEGASEENVVPVQLQSN 764
DB 721 LCEDPSGAGVPRTLNPNVLASPPKDEDEGASEENVVPVQLQSN 764

RESULT 6
US-10-473-127-761
; Sequence 761, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 761
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-761

Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSSPVFRLETLDDGGQEDGSEADRGKLDGSGGLPPMESQFGEDRKFAQIRVNLNY 60
DB 1 MTSPPSSPVFRLETLDDGGQEDGSEADRGKLDGSGGLPPMESQFGEDRKFAQIRVNLNY 60
QY 61 RKG TGASQDPNRRDRDLFNAVSRGVDPDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
DB 61 RKG TGASQDPNRRDRDLFNAVSRGVDPDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRGRHSALHIAIEKRSIQCVK 180
DB 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRGRHSALHIAIEKRSIQCVK 180
QY 181 LIVENGANVHARACGFFQKGQCTCFYFGLPLSLAAC TKQWDVVSYLENPHOPASLOA 240
DB 181 LIVENGANVHARACGFFQKGQCTCFYFGLPLSLAAC TKQWDVVSYLENPHOPASLOA 240
QY 241 TDSQGNVTLHALVMISDNSAENIALVTSMDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300
DB 241 TDSQGNVTLHALVMISDNSAENIALVTSMDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300
```



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QY 61 RKGTSQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
Db 61 RKGTSQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYGRGSHALHIAIEKRSIQCVK 180
Db 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYGRGSHALHIAIEKRSIQCVK 180
QY 181 LLVENGANVHARACGRFFQKGQGTCTFYFGEPLPLSLAACTKQWDVVSYLENPHOPASLOA 240
Db 181 LLVENGANVHARACGRFFQKGQGTCTFYFGEPLPLSLAACTKQWDVVSYLENPHOPASLOA 240
QY 241 TDSQGNVTVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPKL 300
Db 241 TDSQGNVTVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPKL 300
QY 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
Db 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
QY 361 HCKSPHRHRMVLEPLNKLLOAKWDLII PKPFNLFLCNLIYMEIFTAVAYHOPTLKKQAA 420
Db 361 HCKSPHRHRMVLEPLNKLLOAKWDLII PKPFNLFLCNLIYMEIFTAVAYHOPTLKKQAA 420
QY 421 PHLKAEVGNMMLTGHIILLLGGIYLLVQWYFMRHRHVFIMISFIDSYPFELLFQALL 480
Db 421 PHLKAEVGNMMLTGHIILLLGGIYLLVQWYFMRHRHVFIMISFIDSYPFELLFQALL 480
QY 481 TVVSQVLCFLAIEWYLLPVLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKVLRLDLRFL 540
Db 481 TVVSQVLCFLAIEWYLLPVLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKVLRLDLRFL 540
QY 541 IYLVFLGPAVALVSLSOEAWRPEATGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600
Db 541 IYLVFLGPAVALVSLSOEAWRPEATGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600
QY 601 FKFTIGMGLAFOBQLHFRGMVLLIIAYVLLTYVILLNMLIALMSETVNSVATDSWSIW 660
Db 601 FKFTIGMGLAFOBQLHFRGMVLLIIAYVLLTYVILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAI SVLEMENGYWCCRKKQAGVMLTVGTGTPDGS PDERWC FRVEEVNWNASWEQTLP 720
Db 661 KLOKAI SVLEMENGYWCCRKKQAGVMLTVGTGTPDGS PDERWC FRVEEVNWNASWEQTLP 720
QY 721 LCEDPGAGVPRTLENPVLASPPKDEDDGASEENYVPVQLLOSN 764
Db 721 LCEDPGAGVPRTLENPVLASPPKDEDDGASEENYVPVQLLOSN 764

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RESULT 7

```

US-10-473-127-762
; Sequence 762, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 762
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-762

Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPSSSPVPRLETLDDGGDEGSEADRGKLDGSGLPMMESQFQGEDRKFAPQIRVNLNY 60
Db 1 MTPSSSPVPRLETLDDGGDEGSEADRGKLDGSGLPMMESQFQGEDRKFAPQIRVNLNY 60
QY 61 RKGTCASQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
Db 61 RKGTCASQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYGRGSHALHIAIEKRSIQCVK 180
Db 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYGRGSHALHIAIEKRSIQCVK 180
QY 181 LLVENGANVHARACGRFFQKGQGTCTFYFGEPLPLSLAACTKQWDVVSYLENPHOPASLOA 240
Db 181 LLVENGANVHARACGRFFQKGQGTCTFYFGEPLPLSLAACTKQWDVVSYLENPHOPASLOA 240
QY 241 TDSQGNVTVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPKL 300
Db 241 TDSQGNVTVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPKL 300
QY 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
Db 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
QY 361 HCKSPHRHRMVLEPLNKLLOAKWDLII PKPFNLFLCNLIYMEIFTAVAYHOPTLKKQAA 420
Db 361 HCKSPHRHRMVLEPLNKLLOAKWDLII PKPFNLFLCNLIYMEIFTAVAYHOPTLKKQAA 420
QY 421 PHLKAEVGNMMLTGHIILLLGGIYLLVQWYFMRHRHVFIMISFIDSYPFELLFQALL 480
Db 421 PHLKAEVGNMMLTGHIILLLGGIYLLVQWYFMRHRHVFIMISFIDSYPFELLFQALL 480
QY 481 TVVSQVLCFLAIEWYLLPVLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKVLRLDLRFL 540
Db 481 TVVSQVLCFLAIEWYLLPVLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKVLRLDLRFL 540
QY 541 IYLVFLGPAVALVSLSOEAWRPEATGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600
Db 541 IYLVFLGPAVALVSLSOEAWRPEATGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600
QY 601 FKFTIGMGLAFOBQLHFRGMVLLIIAYVLLTYVILLNMLIALMSETVNSVATDSWSIW 660
Db 601 FKFTIGMGLAFOBQLHFRGMVLLIIAYVLLTYVILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAI SVLEMENGYWCCRKKQAGVMLTVGTGTPDGS PDERWC FRVEEVNWNASWEQTLP 720
Db 661 KLOKAI SVLEMENGYWCCRKKQAGVMLTVGTGTPDGS PDERWC FRVEEVNWNASWEQTLP 720
QY 721 LCEDPGAGVPRTLENPVLASPPKDEDDGASEENYVPVQLLOSN 764
Db 721 LCEDPGAGVPRTLENPVLASPPKDEDDGASEENYVPVQLLOSN 764

```

RESULT 8

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US-10-473-127-765
; Sequence 765, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26

```



```
QY 541 IYLVFLGFAVALVSLQSAWRPEAFTGNATESVQPMGQDEGNGAQRGILEASLEL 600
DB 541 IYLVFLGFAVALVSLQSAWRPEAFTGNATESVQPMGQDEGNGAQRGILEASLEL 600
QY 601 FKFTTGMGELAFQEQHLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTTGMGELAFQEQHLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAI SVLEMENGYWCRKQKQAGVMLTVGTPDGS PDERWC FRVEEVNWNASWEQTLP 720
DB 661 KLOKAI SVLEMENGYWCRKQKQAGVMLTVGTPDGS PDERWC FRVEEVNWNASWEQTLP 720
QY 721 LCEDPGAGVPRTLENPVLASPPKEDGCGASENNYVPVQLQSN 764
DB 721 LCEDPGAGVPRTLENPVLASPPKEDGCGASENNYVPVQLQSN 764

RESULT 10
US-10-473-127-772
; Sequence 772, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 772
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-772

Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSSPVFRLETLDGQDGSADRGKLD FGSGLPPMESQFGEDRKFPQIRVNLNY 60
DB 1 MTSPPSSPVFRLETLDGQDGSADRGKLD FGSGLPPMESQFGEDRKFPQIRVNLNY 60
QY 61 RKG TGASQPDNRPDRDRRLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
DB 61 RKG TGASQPDNRPDRDRRLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
QY 121 MKAVLNKDGYNACILPLQIDRDSGNPQPLVNAQCTDDYYRHSALHIAIEKRSLOCVK 180
DB 121 MKAVLNKDGYNACILPLQIDRDSGNPQPLVNAQCTDDYYRHSALHIAIEKRSLOCVK 180
QY 181 LLVENGANVHARACGRFFKQGGTCFYFGEPLSLAACKQWVSVYLLNPHQPASLOA 240
DB 181 LLVENGANVHARACGRFFKQGGTCFYFGEPLSLAACKQWVSVYLLNPHQPASLOA 240
QY 241 TDSQNTVHALVMSIDNSAENIALVTSWYDGLLQAGARLCTPTVOLEDIRNLQDLTPKL 300
DB 241 TDSQNTVHALVMSIDNSAENIALVTSWYDGLLQAGARLCTPTVOLEDIRNLQDLTPKL 300
QY 301 AAKEGKIEIFRHILQREFSGLSLRSKFTWCYGPVRVSLYDLASVDSCEENSYLEIIAF 360
```

```
DB 301 AAKEGKIEIFRHILQREFSGLSLRSKFTWCYGPVRVSLYDLASVDSCEENSYLEIIAF 360
QY 361 HCKSPHRHRMVMVLEPLNKLQAKWDLIPKPFNLFCNLIYNFI FTAVAYHPTLKKQAA 420
DB 361 HCKSPHRHRMVMVLEPLNKLQAKWDLIPKPFNLFCNLIYNFI FTAVAYHPTLKKQAA 420
QY 421 PHLKA EVGNSMLLTGHILILGGIYLLVGQWYFWRRHVFIWISFIDS YFEILFPOALL 480
DB 421 PHLKA EVGNSMLLTGHILILGGIYLLVGQWYFWRRHVFIWISFIDS YFEILFPOALL 480
QY 481 TVVSQVLCFLAEWVLP LLSVALVGLWNLNLYYTRGFQHTGIYSVMIOKVILRDLRLFL 540
DB 481 TVVSQVLCFLAEWVLP LLSVALVGLWNLNLYYTRGFQHTGIYSVMIOKVILRDLRLFL 540
QY 541 IYLVFLGFAVALVSLQSAWRPEAFTGNATESVQPMGQDEGNGAQRGILEASLEL 600
DB 541 IYLVFLGFAVALVSLQSAWRPEAFTGNATESVQPMGQDEGNGAQRGILEASLEL 600
QY 601 FKFTTGMGELAFQEQHLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTTGMGELAFQEQHLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAI SVLEMENGYWCRKQKQAGVMLTVGTPDGS PDERWC FRVEEVNWNASWEQTLP 720
DB 661 KLOKAI SVLEMENGYWCRKQKQAGVMLTVGTPDGS PDERWC FRVEEVNWNASWEQTLP 720
QY 721 LCEDPGAGVPRTLENPVLASPPKEDGCGASENNYVPVQLQSN 764
DB 721 LCEDPGAGVPRTLENPVLASPPKEDGCGASENNYVPVQLQSN 764

RESULT 11
US-10-473-127-776
; Sequence 776, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-776

Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSSPVFRLETLDGQDGSADRGKLD FGSGLPPMESQFGEDRKFPQIRVNLNY 60
DB 1 MTSPPSSPVFRLETLDGQDGSADRGKLD FGSGLPPMESQFGEDRKFPQIRVNLNY 60
QY 61 RKG TGASQPDNRPDRDRRLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
DB 61 RKG TGASQPDNRPDRDRRLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
```

```
QY 121 MKAVLNLDKGVNACILPLQIDRDSGNPQPLVNAOCTDDYYRGHSALHIAIEKRSQCVR 180
Db 121 MKAVLNLDKGVNACILPLQIDRDSGNPQPLVNAOCTDDYYRGHSALHIAIEKRSQCVR 180
QY 181 LLVENGANVHARACGRFFQKGQCTCFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
Db 181 LLVENGANVHARACGRFFQKGQCTCFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
QY 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLDLTPKL 300
Db 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLDLTPKL 300
QY 301 AAKEGKIEIPRHILQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
Db 301 AAKEGKIEIPRHILQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
QY 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKFFLNFLCNLIYMFIFTAVAYHQP TLKQAA 420
Db 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKFFLNFLCNLIYMFIFTAVAYHQP TLKQAA 420
QY 421 PHLKAEGVSNMLTGHILILGGIYLLVQGLWYFRRHVFIWISFIDSYPFILLFQALL 480
Db 421 PHLKAEGVSNMLTGHILILGGIYLLVQGLWYFRRHVFIWISFIDSYPFILLFQALL 480
QY 481 TVVSQVLCFLAIEWYLPLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVIIRDLLRFL 540
Db 481 TVVSQVLCFLAIEWYLPLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVIIRDLLRFL 540
QY 541 IYLVFLGFAVALVSLSQEAWRPEAPGTGNATESVQPMQEGDEGNGAQRGILEASLEL 600
Db 541 IYLVFLGFAVALVSLSQEAWRPEAPGTGNATESVQPMQEGDEGNGAQRGILEASLEL 600
QY 601 FKFTIGMGLAFQEOQLHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
Db 601 FKFTIGMGLAFQEOQLHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLQKAI SVLEMENGYWCKKQKQAGVMLTVGTGPDGSPDRWCFCFRVEEVNWSWEGTLPT 720
Db 661 KLQKAI SVLEMENGYWCKKQKQAGVMLTVGTGPDGSPDRWCFCFRVEEVNWSWEGTLPT 720
QY 721 LCEDPGAGVPRTELENPVLASPPKDEBDGASENYPVQLQSN 764
Db 721 LCEDPGAGVPRTELENPVLASPPKDEBDGASENYPVQLQSN 764
```

RESULT 12

```
US-10-473-127-779
; Sequence 779, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 779
; LENGTH: 764
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-473-127-779
```

```
Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MTSPPSSPVFRLIETLDGGQEDGSEADRGKLDGSGGLPPMESQFQGEDRKPFAQIRVNLNY 60
Db 1 MTSPPSSPVFRLIETLDGGQEDGSEADRGKLDGSGGLPPMESQFQGEDRKPFAQIRVNLNY 60
QY 61 RKGTCASQDPDRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSTYTGSGTKTCL 120
Db 61 RKGTCASQDPDRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSTYTGSGTKTCL 120
QY 121 MKAVLNLDKGVNACILPLQIDRDSGNPQPLVNAOCTDDYYRGHSALHIAIEKRSQCVR 180
Db 121 MKAVLNLDKGVNACILPLQIDRDSGNPQPLVNAOCTDDYYRGHSALHIAIEKRSQCVR 180
QY 181 LLVENGANVHARACGRFFQKGQCTCFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
Db 181 LLVENGANVHARACGRFFQKGQCTCFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
QY 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLDLTPKL 300
Db 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLDLTPKL 300
QY 301 AAKEGKIEIPRHILQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
Db 301 AAKEGKIEIPRHILQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
QY 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKFFLNFLCNLIYMFIFTAVAYHQP TLKQAA 420
Db 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKFFLNFLCNLIYMFIFTAVAYHQP TLKQAA 420
QY 421 PHLKAEGVSNMLTGHILILGGIYLLVQGLWYFRRHVFIWISFIDSYPFILLFQALL 480
Db 421 PHLKAEGVSNMLTGHILILGGIYLLVQGLWYFRRHVFIWISFIDSYPFILLFQALL 480
QY 481 TVVSQVLCFLAIEWYLPLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVIIRDLLRFL 540
Db 481 TVVSQVLCFLAIEWYLPLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVIIRDLLRFL 540
QY 541 IYLVFLGFAVALVSLSQEAWRPEAPGTGNATESVQPMQEGDEGNGAQRGILEASLEL 600
Db 541 IYLVFLGFAVALVSLSQEAWRPEAPGTGNATESVQPMQEGDEGNGAQRGILEASLEL 600
QY 601 FKFTIGMGLAFQEOQLHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
Db 601 FKFTIGMGLAFQEOQLHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLQKAI SVLEMENGYWCKKQKQAGVMLTVGTGPDGSPDRWCFCFRVEEVNWSWEGTLPT 720
Db 661 KLQKAI SVLEMENGYWCKKQKQAGVMLTVGTGPDGSPDRWCFCFRVEEVNWSWEGTLPT 720
QY 721 LCEDPGAGVPRTELENPVLASPPKDEBDGASENYPVQLQSN 764
Db 721 LCEDPGAGVPRTELENPVLASPPKDEBDGASENYPVQLQSN 764
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RESULT 13

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US-10-915-017-36
; Sequence 36, Application US/10915017
; Publication NO. US20050095650A1
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: UCSF-084CON2
; CURRENT APPLICATION NUMBER: US/10/915,017
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; CURRENT FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 09/978,303
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-915-017-36

Query Match      100.0%; Score 4004; DB 17; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTPSSSPVFRLETLDDGGQDGSADRGKLDGSGLPPMESQFQGEDRKFAPIQIRVNLNY 60
Db 1 MTPSSSPVFRLETLDDGGQDGSADRGKLDGSGLPPMESQFQGEDRKFAPIQIRVNLNY 60
Qy 61 RKGTCASQPDNRRDRLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
Db 61 RKGTCASQPDNRRDRLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
Qy 121 MKAVLNLDKGVNACILPLQLQIDRDSGNPQLVNAQCTDDYYRGHSALHAIATEKRSLOCVK 180
Db 121 MKAVLNLDKGVNACILPLQLQIDRDSGNPQLVNAQCTDDYYRGHSALHAIATEKRSLOCVK 180
Qy 181 LLVENGANVHARACGRFQKQGCTCFYFGEPLPLSLAACTKQWDVVSYLLENPHOPASLOA 240
Db 181 LLVENGANVHARACGRFQKQGCTCFYFGEPLPLSLAACTKQWDVVSYLLENPHOPASLOA 240
Qy 241 TDSQGNTVLHALVMI SDNSAENIALVTSWYDGLLQAGARLCTPVOLEDIRNLQDLTPKL 300
Db 241 TDSQGNTVLHALVMI SDNSAENIALVTSWYDGLLQAGARLCTPVOLEDIRNLQDLTPKL 300
Qy 301 AAKGKKEIFRHILQREPSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSULEIIAF 360
Db 301 AAKGKKEIFRHILQREPSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSULEIIAF 360
Qy 361 HCKSPHRRMWVLEPLNKLQAKWDLLIPKFPLNPLCNLIYMFIFTAVAYHOPTLKQAA 420
Db 361 HCKSPHRRMWVLEPLNKLQAKWDLLIPKFPLNPLCNLIYMFIFTAVAYHOPTLKQAA 420
Qy 421 PHLKAEVGNMLLTGHILILGGLVLLGQWYFWRRHVFVWISPIDSVERTFLFQALL 480
Db 421 PHLKAEVGNMLLTGHILILGGLVLLGQWYFWRRHVFVWISPIDSVERTFLFQALL 480
Qy 481 TVWSQVLCFLAEWYLPPLLVSALVLGWNLLYYTRGFQHTGTIGYSYMWIKQVILRDLRLFL 540
Db 481 TVWSQVLCFLAEWYLPPLLVSALVLGWNLLYYTRGFQHTGTIGYSYMWIKQVILRDLRLFL 540
Qy 541 IYLVPLFGFAVALVSLSQEAWRPEAPTGNATATESVQPMEGQDEGNGAQYRGILEASLEL 600
Db 541 IYLVPLFGFAVALVSLSQEAWRPEAPTGNATATESVQPMEGQDEGNGAQYRGILEASLEL 600
Qy 601 PKFTTGMGELAFQEQLHFRGMVLLLLIAYVLLTYTLLNMLLTALMSETVNSVATDSWSTW 660
Db 601 PKFTTGMGELAFQEQLHFRGMVLLLLIAYVLLTYTLLNMLLTALMSETVNSVATDSWSTW 660
Qy 661 KLOKAI SVLENMGYVWCKKQKQAGVMLTVGTGKPDGSPDERWCFCRVEEVNMAWSEQTLLPT 720
Db 661 KLOKAI SVLENMGYVWCKKQKQAGVMLTVGTGKPDGSPDERWCFCRVEEVNMAWSEQTLLPT 720
Qy 721 LCEDPSGAGVPRTLNPNVLASPPKDEDEGASENTVPVOLLQSN 764
Db 721 LCEDPSGAGVPRTLNPNVLASPPKDEDEGASENTVPVOLLQSN 764

```

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US-11-013-090-5
; Sequence 5, Application US/11013090
; Publication No. US20050158827A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Curtiss, Rory A.J.
; TITLE OF INVENTION: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
; TITLE OF INVENTION: RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
; FILE REFERENCE: MP198-093P2RCP3DV1AM
; CURRENT APPLICATION NUMBER: US/11/013,090
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: US 09/439,165
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/421,134
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 09/258,633
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 60/114,078
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/108,322
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-013-090-5

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QY 601 FKFTTGMGELAFQEQHFRGMVLLLLAVVLLTYILLNNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTTGMGELAFQEQHFRGMVLLLLAVVLLTYILLNNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAIISVLEMENGYWCRKQKORAGVMLTVGTPDGSPPDERMCFRVEEVNMAWSEOTLPT 720
DB 661 KLOKAIISVLEMENGYWCRKQKORAGVMLTVGTPDGSPPDERMCFRVEEVNMAWSEOTLPT 720
QY 721 LCEDPSGAGVPRTLENPVLASPPKEDDGDGASEENYVPVQLQSN 764
DB 721 LCEDPSGAGVPRTLENPVLASPPKEDDGDGASEENYVPVQLQSN 764

RESULT 15
US-10-168-651-3
; Sequence 3, Application US/10168651
; Publication No. US20030171275A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: YANG, Junming
; APPLICANT: REDDY, Roopa
; APPLICANT: LAL, Preeti
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Danniell B.
; APPLICANT: YAO, Monique G.
; APPLICANT: GANDHI, Ameen R.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Farrah A.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0005 PCT
; CURRENT APPLICATION NUMBER: US/10/168,651
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,000; 60/176,083; 60/177,332; 60/178,572; 60/179,758; 60/181,625
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-21; 2000-01-28; 2000-02-02; 2000-02-10
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030171275A1 2446438CD1
US-10-168-651-3

Query Match 99.9%; Score 3998; DB 14; Length 764;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSFSSPVFRLETLDGQGDGSEADRGKLDGSGGLPPMESQFQGEDRKFPQIRVNLNY 60
DB 1 MTSFSSPVFRLETLDGQGDGSEADRGKLDGSGGLPPMESQFQGEDRKFPQIRVNLNY 60
QY 61 RKGTGASQDPNFRDRRLFNVAHSVGPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
DB 61 RKGTGASQDPNFRDRRLFNVAHSVGPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
QY 121 MKAVLNKQGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRGHSALHTAIEKRSLOQVK 180
DB 121 MKAVLNKQGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRGHSALHTAIEKRSLOQVK 180
QY 181 LLVENGANVHARACGRFFQKQGCTCFYFGELPLSLAACTKQWDVSVSYLLENPHQPASLOA 240
DB 181 LLVENGANVHARACGRFFQKQGCTCFYFGELPLSLAACTKQWDVSVSYLLENPHQPASLOA 240

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QY 241 TDSQNTVVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCPTVOLEDIRNLODITPLKL 300
DB 241 TDSQNTVVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCPTVOLEDIRNLODITPLKL 300
QY 301 AAKEGKIIFRHILOREFSGLSHLRKTEWCYGPVRVSLYDLASVDSCEENSVELEIAF 360
DB 301 AAKEGKIIFRHILOREFSGLSHLRKTEWCYGPVRVSLYDLASVDSCEENSVELEIAF 360
QY 361 HCKSPHRHRMVVLEPLNKLLOAKWDLIIPKPFNLNLIYMFIFTAVAYHQTLLKQAA 420
DB 361 HCKSPHRHRMVVLEPLNKLLOAKWDLIIPKPFNLNLIYMFIFTAVAYHQTLLKQAA 420
QY 421 PHLKAEGNSMLLTGHIILILGGIYLLVQOLWYFRRHVFIWISFIDSFEILFQALL 480
DB 421 PHLKAEGNSMLLTGHIILILGGIYLLVQOLWYFRRHVFIWISFIDSFEILFQALL 480
QY 481 TVVSQVLCFLAIEWYLLPLLSALVLGWLNLNLYYTRGFQHTGIYSVMIQKVILRDLRLFLL 540
DB 481 TVVSQVLCFLAIEWYLLPLLSALVLGWLNLNLYYTRGFQHTGIYSVMIQKVILRDLRLFLL 540
QY 541 IYLVFLPGFAVALVSLSQEAWRPEAPTGPFNATESVQPMEGQDEGNGAQYRGILEASLEL 600
DB 541 IYLVFLPGFAVALVSLSQEAWRPEAPTGPFNATESVQPMEGQDEGNGAQYRGILEASLEL 600
QY 601 FKFTTGMGELAFQEQHFRGMVLLLLAVVLLTYILLNNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTTGMGELAFQEQHFRGMVLLLLAVVLLTYILLNNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAIISVLEMENGYWCRKQKORAGVMLTVGTPDGSPPDERMCFRVEEVNMAWSEOTLPT 720
DB 661 KLOKAIISVLEMENGYWCRKQKORAGVMLTVGTPDGSPPDERMCFRVEEVNMAWSEOTLPT 720
QY 721 LCEDPSGAGVPRTLENPVLASPPKEDDGDGASEENYVPVQLQSN 764
DB 721 LCEDPSGAGVPRTLENPVLASPPKEDDGDGASEENYVPVQLQSN 764

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Search completed: October 5, 2005, 11:37:13  
Job time : 171 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 5, 2005, 11:13:10 ; Search time 20 Seconds  
(without alignments)  
3675.480 Million cell updates/sec

Title: US-09-445-614B-2  
Perfect score: 4004  
Sequence: 1 MTPSSSPVRLTLGGQE.....EDEDGASENYPVQLQSN 764

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1652	41.3	838	2 T09054	capsaicin receptor
2	1651.5	41.2	839	2 JC7621	capsaicin receptor
3	634	15.8	725	2 JC7531	calcium transport
4	615.5	15.4	727	2 JC7796	epithelial calcium
5	581	14.5	723	2 JC7795	epithelial calcium
6	414	10.3	900	2 T33026	hypothetical prote
7	382.5	9.8	790	2 T20312	hypothetical prote
8	365.5	9.1	957	2 D88651	protein B0212.5 [i
9	364	9.1	937	2 T37241	olfactory channel
10	261	6.5	519	2 T24772	hypothetical prote
11	209	5.2	1188	2 T19552	hypothetical prote
12	197.5	4.9	1124	2 JH0588	calmodulin-binding
13	191	4.8	1274	2 JN0058	trp protein - fru
14	190.5	4.8	1275	2 J00092	trp protein - fru
15	174	4.3	810	2 T38361	trp protein - hu
16	167.5	4.2	934	1 H71274	probable ankyrin -
17	157.5	3.9	481	2 T23729	hypothetical prote
18	157	3.9	1549	2 T13940	ankyrin - fruit fl
19	151	3.8	1765	2 T42714	ankyrin 3, splice
20	151	3.8	1940	2 T42715	ankyrin 3, splice
21	151	3.8	1943	2 T42713	ankyrin 3, splice
22	151	3.8	1961	2 T42716	ankyrin 3, splice
23	151	3.8	3924	2 S73431	ankyrin 2, neuroa
24	150.5	3.8	793	2 S86238	trp-1 protein - hu
25	150	3.7	887	2 T03939	potassium channel
26	150	3.7	4377	2 A55575	ankyrin 3, long sp
27	147	3.7	1001	2 S30385	G9a protein - huma
28	145.5	3.6	899	2 F88391	protein R06810.4 [
29	144.5	3.6	2004	2 D88948	protein ZK1005.1 [

RESULT 1  
T09054  
capsaicin receptor - rat  
N;Alternate names: vanilloid receptor subtype 1  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T09054  
R;Caterina, M.J.; Schumacher, M.A.; Tominaga, M.; Rosen, T.A.; Levine, J.D.; Julius, D.  
Nature 389, 816-824, 1997  
A;Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway.  
A;Reference number: Z16539; MUID:98007969; PMID:9349813  
A;Accession: T09054  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-838 <CAT>  
A;Cross-references: UNIPROT:Q35433; EMBL:AF029310; NID:G2570932; PIDN:AAC53398.1; PID:G  
A;Experimental source: dorsal root ganglion  
C;Keywords: ion channel; receptor

Query Match 41.3%; Score 1652; DB 2; Length 838;  
Best Local Similarity 46.3%; Pred. No. 5.5e-120;  
Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;

Qy	18	GOEDGSADRGKLDGSGSLPPMESQFOGEDRKFAPIQIRVN---	LNRYKRGTG-----	65
Db	51	GKGDSEAS-----	PLDCPYEEGLASCPITVSSVLTIQRPDGPASVRPSSQ	99
Qy	66	-----ASQPDNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSYTEGSGTKTCLM	121	
Db	100	DSVSAGEKPPRLYDRRSIFDAVAQSNCOELESLLPFLQRSKGLTDSFKDPETGKTCLL	159	
Qy	122	KAVNLKDGYNACILPLQLDRDGSNPQPLVNAOCTDDYRGHSALHIAIEKRSLOCVKL	181	
Db	160	KAMLNHNGQNDTIALLDLVARKTDSLQFVNASYSDSYGQTALHIAIERRWLTVL	219	
Qy	182	LVENGANVHARACGRPFQKGQ--TCFYFGLPLSLAACTQMDVWVSVYLLNPHOPASLOA	240	
Db	220	LVENGADVQAANGDFPKTKGRPGFYFGLPLSLAACTNQLAIVKFLQNSWQPADISA	279	
Qy	241	TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLLQAGARLCPVTQLEDIRNLQDLTPLKL	300	
Db	280	RDSVGNVTLHALVEADVNTDNTKFTVSMYNEILLGAKLHPTLKLBEITNRKGLTPLAL	339	
Qy	301	AAKEGKTEIFRHILQREF--SGLSHLSRKFTWCYGVPRVSVLSYDLASVDSCEENSVLBEI	358	
Db	340	AASGKIGVLAIFYLQREIHEPECHLSRKFTWAGVPVHSSVLSYDLSCIDTCEKNSVLEVI	399	
Qy	359	AF-HCKSPHRRHVVLEPLNKLQAKWDLIPK--FFLNFLCNLIYMFIFTAVAYHQPTLK	416	
Db	400	AYSSSTPNRHDMLLVLEPLNLLQDKWDRFVKRIFYFNFFVYCLYMIIFTAAAYRVPV--	457	
Qy	417	KQAAAP--HLKAEVGNMMLLTGHIILLGGIYLLVQLWYFWRRHVFVWISFIDSFYELLF	474	

ALIGNMENTS



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Db 458 -EGLPPYKQNTVGDYFRVTGEILSVGGVYFFRGIQPLQRPRLSKLSLFDVDSYEILP 516
QY 475 LFOALTYVVSQVLCFLAIEAWYLLVSLVGLWLNLLYTRGFQHTGTGIYSVMIQVILRD 534
Db 517 FVQSLFWLVSVLYFSQRKEYVASVFLSANGTWNNLYYTRGFQNGGIYAVMIEKMLAD 576
QY 535 LIRFLIYLVFLPGFAVALVLSQEAWRPEAPFGPNATESVQPMGEQDEGNGA----- 588
Db 577 LCRFMFVLVFLFGFSTAVVTIED-----GKN---NSLPMESTPHKCRGSACKGN 625
QY 589 QYRGILEASLEFKFTIGMGLAFOQLHFRGMVLLLLAYVLLTYILLNMLIALMSGT 648
Db 626 SYNSLSYTCLELFPKFTIGMGLAFOQLHFRGMVLLLLAYVLLTYILLNMLIALMSGT 685
QY 649 VNSVATDSWSIWKLQKAIISVLEMGYWWC-RKKQAGVWMLTVGTPDGSPPDERWCFRVE 707
Db 686 VNKIAQESKNWIKLQRAITILDTEKSLFKMKRKAFRSGKLLQVGFPPDGKDDYRWCFRVD 745
QY 708 EVNWASWEQTLPTLCDDPSGA-GVPRTLNPNVLASPPKDEDEGASENVVPVOLLQ 762
Db 746 EVNWTNTNNGIINEDPGNCEGVKRTLSFSLRSG----RVSGRNKNFALVPLLR 797

RESULT 2
JC7621
capsaicin receptor, VR1 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7621
R;Crichton, D.N.; Crandall, M.; Sanchez, J.F.; Zou, T.; Krause, J.E.; White, G.
Biochem. Biophys. Res. Commun. 281, 1183-1189, 2001
A;Title: The tissue distribution and functional characterization of human VR1.
A;Reference number: JC7621; MUID:21139751; PMID:11243859
A;Contents: Dorsal root ganglia
A;Accession: JC7621
A;Molecule type: mRNA
A;Residues: 1-839 <OR>
A;Cross-references: UNIPROT:Q9H304; GB:AF196175
C;Comment: This receptor, a transmembrane protein with many phosphorylation sites, is a
its integrative activation by several noxious stimuli, and plays an important role in ir
C;Genetics:
A;Gene: vr1
A;Map position: 17p13
C;Keywords: transmembrane protein
F;201-233/Domain: ankyrin #status predicted <ANK1>
F;248-280/Domain: ankyrin #status predicted <ANK2>
F;333-365/Domain: ankyrin #status predicted <ANK3>
F;433-455/Domain: transmembrane #status predicted <TM1>
F;477-495/Domain: transmembrane #status predicted <TM2>
F;508-531/Domain: transmembrane #status predicted <TM3>
F;543-569/Domain: transmembrane #status predicted <TM4>
F;578-597/Domain: transmembrane #status predicted <TM5>
F;624-644/Region: pore loop #status predicted
F;656-684/Domain: transmembrane #status predicted <TM6>

Query Match 41.2%; Score 1651.5; DB 2; Length 839;
Best Local Similarity 48.5%; Pred. No. 6.1e-120;
Matches 344; Conservative 122; Mismatches 199; Indels 45; Gaps 11;

QY 74 FDRRLFNVAVRGVPEDLAGLPYLSKTYLTDSEYTEGSTGKTCLMKAVLNLDGVNA 133
Db 113 YDRRSIFEAVANNQCDLESLLFLQSKKHLTDNEFKDPTGKTCLLKAMLNLDGQNT 172
QY 134 CILPLQLDRDGNPQPLVNAQCTDDYRGHSHALHTAEKRSLOQVKLLVENCANYHARA 193
Db 173 TIPLLIEARQTLUSKELVNASYTDSTYKQGTALHAIERNNALVTLLVENGADYQAAA 232
QY 194 CGRFFQKQGC-TCFYFGELPLSLAACTKQWDVVSYLENPHQPASLQATDSQGNTVLHAL 252
Db 233 HGDFFKTKRPGFYGELPLSLAACTNQLGIVKFLQNSWQTADISARDSVGNTVLHAL 292
QY 253 VMTSDNSAENIALVTSYMDGLLQAGRLCFTVQLEDIRNLQDLTPLKLAKEGKIEIFRH 312
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```
Db 293 VEVAQNTADNTKFTVSMNEILMLGAKLHPTLKLEELTNKKGMTPLAALAGTGKGLVAY 352
QY 313 ILQREFS--GLSHLSRKRTWCYGPVRVSLVDLASVDSCEENSVLEIIAF-HCKSPHRRH 369
Db 353 ILQREIQBPCECHLSRKFTWAYGVPVHSSLYDLSCIDTCEKNSVLEIAYSSSETPNRHD 412
QY 370 MVVLEPLNKLQAKWDLIPK-FFLNFLCNLIYMEIFTAVAHQPTLKQAAAPHLKAE-V 427
Db 413 MLLVEPLNRLLDQKWRFRVKRIFYENFLVYCLYMIIFTMAAYRPRV--DGLPPPFMEKI 469
QY 428 GNSMLLTGHILLGIGIYLLVGQLWYFWRRHVFIIWISFIDSYFEILLFQALLTVVSQVL 487
Db 470 GYFRTVGEILSVLGGVTFPFGIOYFLQRRPSMKTFLVDSYSEMLFFLOSLFMLATVVL 529
QY 488 CFALAEWLPLLVASVALVGLWLNLLYYTRGFQHTGTGIYSVMIQVILRDLLRFLIYLVFL 547
Db 530 YFSLKEVVASVMSFSLALGWTNMLYYTRGFQMGIVAVMIEKMLILRDLCRFMFVIVFLF 589
QY 548 GFAVALVLSQEA-----WRPEAPTGNATESVQPMGEQDEGNGAQYRGIL 594
Db 590 GFSTAVVTIIEDGKNDSLPSSESTSHRWGPACRPDSS-----YNSLY 632
QY 595 EASLELFKFTIGMGLAFOQLHFRGMVLLLLAVVLLTYILLNMLIALMSSETVNSVAT 654
Db 633 STCLSELFKFTIGMGLAFOQLHFRGMVLLLLAVVLLTYILLNMLIALMSGETVNKIAQ 692
QY 655 DSWSIWKLQKAIISVLEMGYWWC-RKKQAGVWMLTVGTPDGSPPDERWCFRVEVNNAS 713
Db 693 ESKNIWKLQRAITILDTEKSLFKMKRKAFRSGKLLQVGYTPDGKDDYRWCFRVDEVNWT 752
QY 714 WQQTUPTLCDDPSGA-GVPRTLNPNVLASPPKDEDEGASEENVVPVOLLQ 762
Db 753 WNTNNGIINEDPGNCEGVKRTLSFSLRSG----RVSGRHRKNFALVPLLR 798

RESULT 3
JC7531
calcium transport protein, Cat1 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7531
R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev, P.M.; Bro
Biochem. Biophys. Res. Commun. 278, 326-332, 2000
A;Title: Human calcium transport protein Cat1.
A;Reference number: JC7531; MUID:20551480; PMID:11097838
A;Accession: JC7531
A;Molecule type: mRNA
A;Residues: 1-725 <PEN>
A;Cross-references: UNIPROT:Q9H296; GB:AF304463
C;Comment: This protein, a member of a family of Ca2+ channels, has a role in cellular
ine and kidney.
C;Genetics:
A;Gene: Cat1
A;Map position: 7q33-34
C;Keywords: calcium channel; calcium transport; intestine; kidney; transmembrane protein

Query Match 15.8%; Score 634; DB 2; Length 725;
Best Local Similarity 29.2%; Pred. No. 5.3e-41;
Matches 187; Conservative 115; Mismatches 243; Indels 96; Gaps 20;

QY 98 LSKTSKYLTDSEYTEGSTGKTCLMKAVLNLDGVNAACILPLQLIDRDSGNPQPLVNAQCT 157
Db 61 LNKLLKYEDCKVHRGAMGETALHTAA--LYDNLEAAVMVM-----EAAPE-LVPEPMT 111
QY 158 DDYRGHSHALHTAEKRSLOQVKLLVENCANYHARACGRFFQKQGTCTFYFGELPLSLAA 217
Db 112 SELYEGQTALHAIERNNALVNNLVALRARRASVSARATGAFRRSPCNLIYFGEHPLSPAA 171
QY 218 CTQKQWDVVSYLENPHQPASLQATDSQGNTVLHALVMTSDNSAENIALVTSYMDGLL--- 274
Db 172 CVNSEIIVRLLEH--GADIRAQSLGNTVLHIL-----QPNKTFACQMYNLLLSYD 223
```

275 QGAGARLCPTVQLEDIRNLQDLTPKLAAKEGKIEIFRHILQREFSGLSHRKFTWCYC 334  
Db RHGDHLQP---LDLVNPHQGLTFPKLAGVEGNTVMFQHLMKQ-----RKHTQMTYG 271  
335 PVRVSLYDLASVDC--EENSVLRIIAPHCKSPHRHRMVLVLEPLNKLQAKWDL--LPKFF 392  
Db PLTSTLYDLTEIDSSGDEQSLELI-ITTKREARQILDQTPVKELVSLKWKRYGRPYFC 330  
393 LNFCLNLIYMPIFTAVAYH---OPTLKQQAAPHLKAEVGNM-----LTGHI 437  
Db MLCAGIALLYIICFTMCCIVRPLKPTNRNRTSPDNTLLQOKLQEAAYMTPKDDIRLVGEL 390  
438 LILLGGIYLLVGQIWFWRHV--FTWISFIDSYFEILFLQALLTVVSOVLFCFLAEWY 495  
Db VTVVIGAIILLVEVPDIFRNGVTRFFGQTILGPFHVLIIITYAFMVLVTVMWKLIISASGE 450  
496 LPLVLSALVGLMNLAYTYRGFTQGIYSVMIQKVLTRDLLRLLIYLVFLGFAVALVS 555  
Db VVPMSPALVLCNWNMYFARGFQWLGPFPTIMIQKMLFGDLMRFCWLMAVVILGFASAFYI 510  
556 LSQEAWRPEAPTGNPNATESVQPMEGDEGNGAQYRGILEASLELPKFTTIGMGEIAPQEB 615  
Db IFQ-----TEDPEELGHFYDYPMALFSTPELF-LTIIDPANYNVD 550  
616 LHRFGWVLLLLLAYVLLTYILLNMLIALMSETVNSVATDSWIMKLOKALISVLEWNGY 675  
Db MYSIITYAFAIATILMLNLIIAMGDTHWRVAHERDELBELRAQIVATTVMLERKL 608  
676 ---WQ-----CRKKORAGVMLTVGTPDGSPDERWCPRVEE 708  
Db PRCLMPRSGICGREYGLG-----DRWFLRVED 635  
RESULT 4  
JC7796  
epithelial calcium channel 2, ECaC2 - mouse  
N/Alternate names: calcium T1; Cat1  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Apr-2002 #sequence\_revision 17-May-2002 #text\_change 09-Jul-2004  
R/Accession: JC7796  
R/Weber, K.; Erben, R.G.; Rump, A.; Adamaki, J.  
Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001  
A/Title: Gene structure and regulation of the murine epithelial calcium channels ECaC1  
A/Reference number: JC7795  
A/Accession: JC7796  
A/Molecule type: DNA  
A/Residues: 1-727 <WEB>  
A/Cross-references: UNIPROT:Q91WD2; GB:AF336378  
C/Comment: This calcium channel plays an important role in active transcellular calcium  
relevant for in vivo calcium homeostasis.  
C/Genetics:  
A:Gene: ECaC2  
A:Map position: 6  
A:Introns: 43/2; 76/1; 117/1; 163/1; 196/1; 253/3; 302/3; 373/3; 402/3; 428/2; 483/3; 520/3  
C/Keywords: calcium channel  
Query Match 15.4%; Score 615.5; DB 2; Length 727;  
Best Local Similarity 28.0%; Pred. No. 1.4e-39;  
Matches 183; Conservative 116; Mismatches 233; Indels 121; Gaps 21;  
Qy 98 LSKTSKYLTDSEYTEGSTGKTCLMKAVLNLDGVNACILPLLQIDRDSGNPQPLVNAQCT 157  
Db LSKLLKFECEGVHORGAMGETALHIAA--LYDNLLEAAWVLM-----EAAPE-LVPEPMT 111  
Qy 158 DDYRGHSALHIAIEKRSLOCVKLLVNGANVHARACGRPFQKGQCTCFYFGEPLSLAA 217  
Db SELYEGQTAHLHIAVINQNVNLRALLARGASVSARATGVSFHYRPHNLIIYGEHPLSFAA 171  
Qy 218 CTQKQWDVVSYLENPHQPASQATDSQNTVHLVMIQNSAENIALVTSYMDGLL--Q 275  
Db CVGSEEVRLIIIEH---GADIRAQDSLGNTVLHIL-----QPNKTFACQMYNLLLSYD 223  
Qy 276 AGARLCPTVQLEDIRNLQDLTPKLAAKEGKIEIFRHILQREFSGLSHRKFTWCYC 335

QY 350 -BENSULBIIAIFCKSPHRRMVLE--PLNKLQAKWDLILPKPLNFCML-----LY 401  
 DB 280 GEELSLELVWSKKKEARQ---ILBQTPVKELVSLKW---KKYQOPYFCLLGALYIFY 332  
 QY 402 MIFETAVAHQOP-----TLKKQAAPHLKAEVGNMMLTGHILILGGIYL 446  
 DB 333 MVCFTTCVYRPLKFRDANRTHVRDNTIMEQSLQEAQYVYQDKIRLVGELVTIGAVII 392  
 QY 447 L-----VGQWYFWRHRHFWIWSFIDSYPEILFLFOALLTVVSVQVLCFLAIEWYLP 497  
 DB 393 LLELEIDIFRVGASRYFGQ-----TVLGGPHVIIITVASIVLLTMAURLTNVNGEVV 445  
 QY 498 LLVSALVGLWNLIIYTRGFQHTGIYSVMQKVLRLDLRLFLIIYLVFLFGFAVALVSLS 557  
 DB 446 PMSMALVGLWCVMYFARGFQMLPPTIMQKMIQKMIQKMIQKMIQKMIQKMIQKMIQKMI 505  
 QY 558 QBAWRPEAFTGNPATESVQPMQEQDEGNGAORYGLEASLELFKFTIGMGLAFOQLH 617  
 DB 506 Q-----TEDPDLGFEFSDYPTAMPSTFELF-ITIIDGPANRYVDLP 545  
 QY 618 FRGMVILLALLAYVLLFYILLNMLMSETVNSVATDSWSIWKLQAKAISVLEMENGYWM 677  
 DB 546 F--MYSVTYATPAIIATLLMLNLFIAMMGDTHWRVAQERDELWRAQVWATTWMLE----- 598  
 QY 678 CRXKQR-----AGVMLTVGTPKDGSPDERKCFRVE-----VNWASW 714  
 DB 599 -RMPRFLMPSRGICCEYGLG-----DRWLFVEHHQBNQPNRYVLYVEAFKSSDK 649  
 QY 715 EOTLPTLCB-DPSGAGVPTLE-NPVLASPPKDEDEGASEENVYPVQLQSN 764  
 DB 650 BEVQEQLEKQPSGTETGLARGSVVLQTPPLSRITSLSNSHRGWEILRN 701  
 RESULT 6  
 T33026  
 hypothetical protein T09A12.3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T33026  
 R:Hawkins, J.; Fulton, B.; Gillam, B.  
 submitted to the EMBL Data Library, February 1998  
 A:Description: The sequence of C. elegans cosmid T09A12.  
 A:Reference number: Z21265  
 A:Accession: T33026  
 A>Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-900 <HAW>  
 A:Cross-references: UNIPROT:O61220; EMBL:AF047660; PIDN:AAC04431.1; GSPDB:GN000022; CESP:  
 A:Experimental source: strain Bristol N2; clone T09A12  
 C:Genetics:  
 A:Gene: CESP:T09A12.3  
 A:Map position: 4  
 A:Introns: 43/2; 86/3; 260/2; 396/3; 424/2; 495/1; 517/3; 553/3; 691/3; 741/3; 780/3; 82  
 Query Match 10.3%; Score 414; DB 2; Length 900;  
 Best Local Similarity 24.2%; Pred. No. 8.6e-24;  
 Matches 183; Conservative 113; Mismatches 253; Indels 206; Gaps 32;  
 QY 61 RKGTGASQDPNRRDRDLFNAVSRGVPEDLAGLPEVLSKTYL-----TDSEYTE 112  
 DB 98 KKGKGS--GPNVLDD--FNQGENVGD-----LKKALKLLGGGKGKGNESKYRE 144  
 QY 113 -----GSTGKTCLMKAVLNKQGNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGH 164  
 DB 145 ISWKLBERGSMGTIIIGCLLHASDTHNALVLKILDY-----YPKLNDIHISEDYF-GL 198  
 QY 165 SALHIAIERSLQCVKLLVNGANVHARACGRFF-----QKQGT----- 204  
 DB 199 SPLHQAIIINTDCKLVYKPLKGLADVNSRCYGAFFCADDQKASRTDSLEHYVELSUKTNY 258  
 QY 205 --CFYGEPLPLSLAACTKQWDVVSYLLENPHQNPASLQATDSQNTVVLHALVMI SDNSASN 262

DB 259 TGNMYLGEYPLSFAACLNPBPESFRLLLAFLKAMP---NAQDTNGNSVLHMCVI-----HEN 310  
 QY 263 IALVTSWYDGLLOAGARLCPTVQLEDINRLQDLTFLKLAKEGKIEIFRHILQRFSGLS 322  
 DB 311 MA---MFKALCEGASL-RTV-----NKQSLSPLLTAAKLAKKEMFDEILLEGDSV- 358  
 QY 323 HLSRKFTWCYGPVRVSLYDLASVDSREN-----SVLEIIIAFHCKSPHRRMVLEP 375  
 DB 359 -----WAYGDASSTAYPLAKIDITINETTGELNEASALSUVVYQVTVHEHLELDGL- 408  
 QY 376 LNKLQAKWDLILPK-FFLNFCLNIYMFIFTAV-----AYHQP-- 413  
 DB 409 LDTLEAKWEAPAKNMIVSPTAFTLYYICFTVTAFTLRPIGFSTEMLTGEMINRYSEPPP 468  
 QY 414 -----TLKKQAP-----HLKAEVGNMMLTGHILILGGIYL 448  
 DB 469 GRYGNSTLQOVKPVINATSRGLVEWSBPLSQCHLRNWDPPDPFANSYIRLVFELFVVI 528  
 QY 449 GQLWYFRRHRHFWIWSFID-----SYFEILFLFOALLT-----VVSVQVLCFLAIEW 494  
 DB 529 GIC-----VQVFDUDFRDIKRGKKNWNVLTAPPAKITFKLTYFLVLAIMPTRACDL 581  
 QY 495 YLFLIV-----SALVGLWNLIIYTRGFQHTGIYSVMQKVLRLDLRLFLIIYLVFLF 547  
 DB 582 SPVLLVVDNVLITVTMTTTHVLYYCRVIRFVGPVLMVYTIATDIFRFLIYIGIFLM 641  
 QY 548 GP--AVALVLSQEAWRPEAFTGNPATESVQPMQEQDE-----NGAQY 590  
 DB 642 GFSQSFLIFLSC--REANVIKKITDQSEASEGSDKNFNLTRQISAYDTAIVKNAEYF 699  
 QY 591 RGLSEASLELF--KFTIGMGLAFOQLHFRGMVL-----LILLAYVLLTYILL 637  
 DB 700 ENVMOSPTEAFVTRTILTIQEPT-----VLYRMLALCPANTVMWIKVVFILFELFVSI 755  
 QY 638 LNMILMSETVNSVATDSWSIWKLQAKAISVLEME 672  
 DB 756 FNMLIAMWTRIVETIFQTGLE-YKQRAQVILMLE 789  
 RESULT 7  
 T20312  
 hypothetical protein F28H7.10 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T20312; T21533  
 R:Matthews, P.  
 submitted to the EMBL Data Library, June 1996  
 A:Reference number: Z19255  
 A:Accession: T20312  
 A>Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-790 <WIL>  
 A:Cross-references: UNIPROT:P90784; EMBL:Z74030; PIDN:CAA98449.1; GSPDB:GN000023; CESP:F2  
 A:Experimental source: clone D1054  
 R:Berts, M.  
 submitted to the EMBL Data Library, May 1996  
 A:Reference number: Z19435  
 A:Accession: T21533  
 A>Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-790 <W12>  
 A:Cross-references: EMBL:Z72508; PIDN:CAA96644.1; GSPDB:GN000023; CESP:F28H7.10  
 A:Experimental source: clone F28H7  
 C:Genetics:  
 A:Gene: CESP:F28H7.10  
 A:Map position: 5  
 A:Introns: 46/2; 89/3; 129/1; 157/1; 201/1; 264/2; 349/3; 406/3; 487/3; 543/2; 580/1; 67  
 Query Match 9.8%; Score 392.5; DB 2; Length 790;  
 Best Local Similarity 25.3%; Pred. No. 3.4e-22;  
 Matches 182; Conservative 106; Mismatches 243; Indels 189; Gaps 35;  
 QY 61 RKGTGASQDP-NRRDRDLFNAVSRGVPEDLAGLPEVLSKTYL-----TDSEY 111

Db 101 KKGKSGNILDPEQOQ-----AENAG---DLKALKLIDGGKGGKSESRYR 147  
Qy 112 E-----GSTGKT---CLMK--AVLNKDGVNACILPLLIQIDSDGNPQP-LVNAQC 156  
Db 148 EMWMSVDERGSMGENLALCLLQGSALHNL-----IARLLNFFPKLINDIC 194  
Qy 157 TDYRGGHSAHIAIKRSLQCCKLVVANGANVHARACGRFF-----KQGGT----- 204  
Db 195 VSEYYGLSPHLAIYNQDAQFTSLRLGADLNQRCYGAFFCADDOKASRTDSLEHFV 254  
Qy 205 -----CFYFGLPLSLAACTKQMDVSVYLLNPHQPSLOATDSQNTVLHALVM 254  
Db 255 ELTKNTNYTSGMYFGYPLSFAICMGCHDLFRMLA---KKANLSAQDTNGNTALH-LCV 310  
Qy 255 ISDNSAENALVTSMDGLLOAGARLCPTVQLEDIRNLQDLPKLAAK-EGKIEIFRHI 313  
Db 311 IHDK-----MDMLDAVLEAGNIT-----RLANKQNLTA/TLAARLAKKTESIOHL 355  
Qy 314 LQREFSGLSH--LSRKFTFW-CYGPVRVSLYDLASVDSCEENSVEIIFAHFC----- 362  
Db 356 --ELMDGLEQIIDEK--WKAYG-----RALWLSLLGFIFFYCCFVCAYML 398  
Qy 363 -----KSPHRRMVV-----LEPLNKLQAKWDLIPKFFLNFLCNLIYMPIFTAVAYHQ 412  
Db 399 RPSSATTEHLTRGRINDDGETESTNSTNYLQWHA-----IDTQCHLMY---YSAPWYWH 449  
Qy 413 PTLKQAAHPKAEVNSMLTGHILLIGGIVLLVQWLYFRRHVFVWISFIDSYPEI 472  
Db 450 GWFPR-----LGCIEITIIYMLFQILLDFGDIRRIGFQKWF-----NPLKAPPK 493  
Qy 473 LFLFQALLTVVSOVLCFLAI---EWYL---PLLVSAVLGMLNLLYTRGFQHTGIYSV 525  
Db 494 LMFKGALFPIIISIPRLACSFHEFFLTINTWAIISILLVTOHFLYKRAIPFVGPFVL 553  
Qy 526 MIQKILRDLRLFLIYVLFPGFAVALVLSQAEWRPEAPTGNATESVQPMQEGDEG 585  
Db 554 MVYTIATDLVRAMIYSIFLVGSQSFYLIFTSERDS-----TAKKIDPM----- 601  
Qy 586 NGAQYRGILB-----ASLELFKFTIGMGELAFQE-----QLHFRGMVLLILLAYVLYTIL 636  
Db 602 -GSEFNIMENPVDALLRTITMIGFVSFLYREMSACDNFMWMIKGLFVIFETFSVIL 660  
Qy 637 LNMMLIATMSETVNSVATDSWSWKLOKASVLEMGYWCCKQKQAGVMLTVGTPDG 696  
Db 661 QFNLLIAMTRTYETIIFL-TRKEWKQWQAQVILMLEGLSPASRKWH-----LLRYTRPTG 715

## RESULT 8

D88651  
protein B0212.5 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: D88651  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes  
A;Reference number: A75000; MUID:9909613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 287, 2012-2018, 1998  
A;Accession: D88651  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-957 <STO>  
A;Cross-references: UNIPROT:O17469; GB:chr\_IV; PIDN:AAC02569.1; PID:g2854148; GSPDB:GNOC000000000  
A;Note: contains similarity to ankyrin repeats  
C;Genetics:  
A;Gene: B0212.5  
A;Map position: 4

Query Match 9.1%; Score 365.5; DB 2; Length 957;  
Best Local Similarity 23.1%; Pred. No. 5.5e-20;  
Matches 169; Conservative 100; Mismatches 267; Indels 197; Gaps 26;

Qy 73 RFDRD--RLFNASRGVPEDLAGLPEYLSKTSKYITDSEYTEGSGTKTCLMKAVLNKDG 130  
Db 46 RPKRGGELINIYERDGEGLKPAE-----EKLLT-ILYDQGNPKLVYSDIYIKWKG 99  
Qy 131 VNACILPLLIQIDRDSGNPQ-----LVNAQ----- 155  
Db 100 VNV-----QLGLSESVDMQOOSRPFKBYHALWLNKRGVEGENLIHLLNREQQVCYIARI 155  
Qy 156 -----CTDDYR-----GHSALHIAIKRSLQCCKLVVANGANVHARACGRFF----- 198  
Db 156 LLKRFPGHNDIYLGDEQFGQSALHLAIVHDDYETVSLNLSKADVNARACGNFFLPEDF 215  
Qy 199 -----KQGGTCFYFGLPLSLAACTKQMDVSVYLLNPHQPSLOATDSQNTVLHAL 252  
Db 216 KLTKNITDYQYA-YGYEYPLAFAACFGNKDIYDLIIQFCAFP-NLQ--DSFGNTILHMC 271  
Qy 253 VMISNSAENALVTSMDGLLOAGARLCPTVQLEDIRNLQDLPKLAAKKEKIEFRH 312  
Db 272 V-----INYSMSYAVRHWAKPAD-----PHVNHAGFTPLTLATKGRKQIFEE 318  
Qy 313 ILQREFSGLSLSRKFTWCYGPVRVSLYDLASVDSCE-----ENSVEIIFAHCKSP 365  
Db 319 MLE-----IMKVEFWRFSDMTCSAYPLNTLDTIQDGSNTYDSALMTVI--NGSTP 367  
Qy 366 HHRMVVLEPLNKLQAKWDLIPKFFLNFLCNLIYMPI-FTAVAHQPTLKQAAAPHLK 424  
Db 368 EHLDMIGSBIQRLADKWKAPAKRKLIERLVLLIVQLITLSIVVYIRPT-----ELPRLY 423  
Qy 425 AEVGNMMLTGHILLIGGIVLLVQWLYFRRHVFVWISFIDSYPEILFLFOALLTV-- 482  
Db 424 MEDPQ-----WDDYINTACELLTILNCIFVGY 451  
Qy 483 -----VSQVLCFLAIEWYL-----PLLVSAVLVG 506  
Db 452 QQLGEIRTOGMGYLNLTAKAPAVCTANFLLLICIFRLMKHHEIALFVFPALPGS 511  
Qy 507 WLNLYYTRGPQHTGIYSVMIQKILRDLRLFLIYVLFPGFAVA--LVSLSQEAWRPE 564  
Db 512 WIFLFFPARSAKLTGPFQVMYISMIAGDMIRFAISAIPLVSPFSQVYFYGVKMDAKOKL 571  
Qy 565 APTGNATESVQPMQEGDEGCAQYRGILEASLELFPKFTIGMGELAFQQLHFRGMVLL 624  
Db 572 EDTNPHACR-----ISGY-----TIYTYNTPPETFITILFRASMGGYDYEESFCANYQALTXT 623  
Qy 625 LLILAYVLLTYILLNMLIALMSETVNSVATDSWSWKLOKA--ISVLEMGYWCCKKQ 682  
Db 624 LFLVYMFVMPIMINILIAMMGNTYTTVIAQAEKAWRQYAIWVLSRVSQ-----KER 678  
Qy 683 RAGVMLTVGTPKD 695  
Db 679 LAASQLEYSIRLD 691

## RESULT 9

T37241  
olfactory channel protein osm-9 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T37241  
R;Colbert, H.A.; Smith, T.L.; Bargmann, C.I.  
J. Neurosci. 17, 8259-8269, 1997  
A;Title: OSM-9, A novel protein with structural similarity to channels, is required for olfactory channel protein osm-9  
A;Reference number: Z21639; MUID:97477445; PMID:9334401  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-937 <COL>  
A;Cross-references: UNIPROT:O17469; EMBL:AF031408; NID:g2642589; PIDN:AAB87064.1; PID:9334401  
C;Genetics:  
A;Gene: osm-9  
A;Map position: IV  
C;Keywords: transmembrane protein



QY 362 -CKSPH-----RHMVVL-----EPLANK-LLOAKWDL 387  
 Db 727 GCKSADEDFKLEKDAQSVASNDVRYKHPLKLMADAEKHLNPLSKALKYKWNRL 786  
 QY 388 -IPKFFLNLFLNLIYFIETAVAYHOPTL-----KKQAAAPHLKAEVGN 430  
 Db 787 GRPMYFALPMYLVFIVSLTQYVYRHTKAPYVWNNSESYDSEYFENETCPQINTTKPD- 845  
 QY 431 MLTGTGHIILGGIYLLVGLQWYFWRHVFI--WISFIDSYFILLFLQ-ALLTVVSQVL 487  
 Db 846 -VVMKIIQTLAVCOILVECFQFORFAYLVNWNEMID-----CFIYSTALITVYDFSE 899  
 QY 488 CF---LAIEMWPLLSVALVGLMNLVYTRGFQHTGIYSVMIQKVILRDLRLFLLIYL 543  
 Db 900 CSATSGVRQWQWQILAAICIFGGINLLFMIRKMPFGFVVMFVDIV-KTFRRFFPVFV 958  
 QY 544 VFLFGFAVALVSLSQEAWRPEAPT---GNPATESVQPMQEGDEGNGAQYRGILEASLEL 600  
 Db 959 LFIIATSSSFVILQN--REFESTIFMSPLKTTVM--MIGE----- 995  
 QY 601 FKFTIGMGEIAFOEQLHFRGN-----VLLLLAVLLTYILLNMLIALMSETVNSV 652  
 Db 996 FEPT--GIFHGDETHAERKMGFGPAHTAVACALFFFCIITILLMNLVGLAVDDIKGV 1052  
 QY 653 ATDSWSIWKLOKALS-VLEME-----NGY--WRCRKK 681  
 Db 1053 -QKAEKLRAMQVDLVLOIEASLSHPFIQTKKYATCRYATFPYKLUHKTGFAGWNSFR 1111  
 QY 682 QRAGVMLTVGTKPD 695  
 Db 1112 RRFQ--LSVSTDPE 1123

## RESULT 12

JH0588  
 Calmodulin-binding protein trpl - fruit fly (Drosophila melanogaster)  
 C;Species: Drosophila melanogaster  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
 C;Accession: JH0588  
 R;Phillips, A.M.; Bull, A.; Kelly, L.E.  
 Neuron 8, 631-642, 1992  
 A;Title: Identification of a Drosophila gene encoding a calmodulin-binding protein with  
 A;Reference number: JH0588; MUID:92232293; PMID:1314616  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-1124 <PHI>  
 A;Cross-references: UNIPROT:P48994; GB:M88185; NID:G469057; PID:G158715  
 A;Experimental source: head  
 C;Genetics:  
 A;Gene: trpl  
 A;Cross-references: FlyBase:FBgn0005614  
 C;Superfamily: TRPC3 protein  
 C;Keywords: calmodulin binding; phosphoprotein; transmembrane protein  
 F;341-362/Domain: transmembrane #status predicted <TM1>  
 F;374-396/Domain: transmembrane #status predicted <TM2>  
 F;462-479/Domain: transmembrane #status predicted <TM3>  
 F;512-533/Domain: transmembrane #status predicted <TM4>  
 F;549-572/Domain: transmembrane #status predicted <TM5>  
 F;643-668/Domain: transmembrane #status predicted <TM6>  
 F;710-727,809-825/Region: calmodulin binding #status predicted  
 F;722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 4.9%; Score 197.5; DB 2; Length 1124;  
 Best Local Similarity 19.7%; Pred. No. 7.6e-07;  
 Matches 162; Conservative 130; Mismatches 281; Indels 249; Gaps 38;  
 QY 131 VNACILPLQLIDRSGNQPL-----VNAQCTDD 159  
 Db 25 VGGCCVPL-----GLPQPLLEBKFPLLAVERGDMPNVRRILQKALRHQINICWDP 77  
 QY 160 YRGHSALHIAIEKRSIQCVKLLVNG-----ANVHARAC-----GRFFQKG 201

Db 78 L--GRRALTALDNENLEMVLLVVMGVETKDALLHAINABFEAVVELLEHEELYKGG 135  
 QY 202 Q-----GTCFYFGEEL-PLSLAACTQMDVWSYLLLEN-----PH-----OPASL 238  
 Db 136 EYYSQKQVDINTAMFADITPLMLAAHKNFILRILLDRGAAPVPHDIRCCBECVRL 195  
 QY 239 QATDSQGNVTLH-----ALVMSIDNSAENIALVTSMDYDGLGLOAGARLCPTVOLED 288  
 Db 196 TAEDSLRHSLSRVNIYRALSPLICTNSDPSSTAFQLSWELRNALTAQECECKSEYMDL 255  
 QY 289 INNLQ-----DLTPLKLAKEGKIEI-----FRHILQRESGLSHLRKRTEWC 332  
 Db 256 RRQCKQFAVDLLDQTRTSNELAIILNYPQMSYBEGDRMSLTRLVQALSYKQKKEV--A 313  
 QY 333 YGPVRVSL-----YDLASVDSCEENSYLEIIAFHCKSPHRRHVMVLEPLNKL-----QAK 383  
 Db 314 HSNIQQLLSIWD--GLPGFRKSIQDKVI--CIA-----QVAVLFPLYCLIYMCAPNCR 365  
 QY 384 WDLILPKFFLNLFCN---LIYMFITAVA-----YHPTLLKQAAPHLKAEVGN 429  
 Db 366 TQQLMRKPPMKFLIHASSYLLFFLILLVSQRADDDFVRIFGTTRMKKELAEQELRQRG 425  
 QY 430 SMLLTGHILILGGIYLLVGLQWYFWRHVFIWISFIDSYFELLFLFOALL--TVVSQVL 487  
 Db 426 ---TPSKLELIWVMYV---IGFVMEBVEQEIFAVGMKSYLRNMWNFIDFLRNSLYVSM 477  
 QY 488 CFLAIEW-----YLP-----LLVSALVGLMNLVLYYTRGFQ 518  
 Db 478 CLRFAFYIOATEIARDPQMAVYIPREKWHDFDQLTAAGLFAAANVFSALKVHLFSINP 537  
 QY 519 HTGIYSVMIQKVIKILRDLRLFLTYLVFLFGFAVALVSLSQEAW-----RPEAPTGNAT 572  
 Db 538 HLGPLQISLGRVI-DIVKFFFIYTLVLFAPA---CGLNQLWYFAALEKSKCVLPQ-- 591  
 QY 573 ESVQPMQEGDENGA-----QYRGILEASLELFPKFTIGMGEI-----AQEQLHFR 619  
 Db 592 ---GEADWGHGSDQMKWRRCGNLFESSQSLEWASFGVMGLDDFELSGLSKSYTRFW 644  
 QY 620 GMVLLALLAVLLTYILLNMLIALMSETVNSVATDSWSIWKLOKALISVLEMENGYWCCR 679  
 Db 645 G--LLMFGSYVINVLNLLTAMNSNYAMIDEHSDTEWKFAR-----TKLWMSY 694  
 QY 680 KQKQAGVMLTVGTPKDGSPDERMCFRV-----EEYNWASWQTLPTLC 722  
 Db 695 FEDSA---TLPPFNVLPVSKVIRIFRKSSTIDRQSKRKEQEQFSEYDINIMRSLV 750  
 QY 723 EDPSGAGVPTLENPVLASPKKEDD--DGASEBNYVPVQLLQ 762  
 Db 751 W-RYVAAHMKRFEN---NPVSEDDINEVKSEINTWRYEMLE 787

## RESULT 13

JN0015  
 trp protein - fruit fly (Drosophila melanogaster)  
 C;Species: Drosophila melanogaster  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 02-Feb-2001  
 C;Accession: JN0015  
 R;Wong, F.; Schaefer, E.L.; Roop, B.C.; LaMendola, J.N.; Johnson-Seaton, D.; Shao, D.  
 Neuron 3, 81-94, 1989  
 A;Title: Proper function of the Drosophila trp gene product during pupal development is  
 A;Reference number: JN0015; MUID:90148782; PMID:2482778  
 A;Accession: JN0015  
 A;Molecule type: mRNA  
 A;Residues: 1-1274 <WON>  
 C;Comment: This photoreceptor membrane-associated protein is not required for the occur  
 C;Genetics:  
 A;Gene: trp  
 A;Cross-references: FlyBase:FBgn0003861  
 A;Map position: 99C5-6  
 C;Superfamily: TRPC3 protein  
 C;Keywords: glycoprotein; nucleotide binding; P-loop; phosphoprotein; transmembrane pro  
 F;1257-1263/Region: nucleotide-binding motif A (P-loop)

F:64,70,899/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:191,602,880,883,924/Binding site: phosphate (Ser) (covalent) #status predicted  
F:800,1266/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 4.8%; Score 191; DB 2; Length 1274;  
Best Local Similarity 20.2%; Pred. No. 2.9e-06;  
Matches 134; Conservative 99; Mismatches 237; Indels 192; Gaps 30;  
F:334-354/Domain: transmembrane #status predicted <TM2>  
F:378-401/Domain: transmembrane #status predicted <TM2>  
F:419-436/Domain: transmembrane #status predicted <TM3>  
F:457-471/Domain: transmembrane #status predicted <TM4>  
F:504-527/Domain: transmembrane #status predicted <TM5>  
F:612-630/Domain: transmembrane #status predicted <TM6>  
F:636-661/Domain: transmembrane #status predicted <TM7>

QY 153 NAOCTDDYRGHSALHIAIEKRSLOCVKLLVNGANVHARACGRFFQKGCTCFYFGEPL 212  
DB 62 NINCTDPNMR--SALISAENENFDMVILLENHIEV-----GDALLHAISEY 108  
QY 213 LSLAACKQWDVSVYLLNPHOPASLOATDSQNT-----VLHLMVMSNSAENIALVTS 268  
DB 109 VEAVEBELLOWEETNH---KEGQPSWEAVDRSKSTFTVDITPLILAAHRNNYILKI---- 162  
QY 269 MYDGLLOAGARL-----CPTVQLED-----IRNLQDLTPLKLAKEG 305  
DB 163 ----LLDRGATLPMHDVKCGDCVTSQTDSLRHSQSRINAYRALSASSIALSSRP 218  
QY 306 KIBIFRHILQREFSGLSHRKFTWCYGPVRVSLYDLAS--VDSCEENSVLBIIFPHCK 363  
DB 219 VLTAFO--LSWELKRLQAMESEFRAE-YTEMQMVQDFGTSLLDHARTSMELEVMNFH 275  
QY 364 SP-----HRRMVVLEP-LNKLLQAKWDLIPKE----- 391  
DB 276 EPSHDIWCLASSETLERLKLAIKYKQTFVAHPNVQQLAAIWDGLPGFPOBASQQLMD 335  
QY 392 FLNFCNLNLYMFIFTAVAVHPTLKKQAAPHLK-AEVDGNSMLTGT-----HILILL 441  
DB 336 VVKLGCSFPYI-----SLKYLAPDSEGAKFMRNPLSSSRTPCSYMFPLMLL 383  
QY 442 GGYLLVAGQL-----WYF-----WRRH-----VF----- 460  
DB 384 GAASLRVQITPELLAPPWMLTMDWRKHERGSLPGPIELAIITVIMALIPEELKSLYS 443  
QY 461 -----IW--ISPIDSYFELFLP--QALLTVVSQVLCFLAIEWYL-----PL 498  
DB 444 DGLFEYIMDLNIVDYISNMFYVTILCRATAWVIVHRDLWFRGIDPYFPREHWHFDDPM 503  
QY 499 LVS-----ALVGLMNLNLYYTRGFQHTGIYSVMIOKVILRDLRLFLLYLVFLGFAVA 552  
DB 504 LLESGAPAGMVFSLKLVHIFINPHLGPLQVSLGRMII-DIIKFFIYTLVLFAG-- 560  
QY 553 LVLSQEAQMRPEAPTGNATESVQPMGEDEGNGA-----QYRGILEASLELFKFTIGM 607  
DB 561 -CGLNQLLWY-YAELEKNKCYHLHPDVADFDQEKACTIWRREFSNLFQSLFWSFGL 618  
QY 608 GELAFQ-----QLHFRGMVLLLLAYVLLTYILLNMLIAMSSETVNSVATDSWSIWKLQ 663  
DB 619 VDLVSFDLAGIKSFTRFWALLMFGYSVINIIVLLNMLIAMNSYQIISERADTEWKFA 678  
QY 664 KA 665  
DB 679 RS 680

RESULT 14  
JU0092  
trp protein - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 17-Nov-2000  
C:Accession: JU0092  
R:Montell, C.; Rubin, G.M.  
Neuron 2, 1313-1323, 1989  
A:Title: Molecular characterization of the Drosophila trp locus: a putative integral mem  
A:Reference number: JU0092; MUID:90180449; PMID:2516726  
A:Accession: JU0092  
A:Molecule type: mRNA  
A:Residues: 1-1275 <MON>  
A:Experimental source: strain Oregon R  
C:Comment: trp protein is expressed predominantly in the rhabdomeric membranes of the ph  
C:Genetics:

A:Gene: trp  
A:Cross-References: FlyBase:FBgn0003861  
C:Superfamily: TRPC3 protein  
C:Keywords: transmembrane protein

F:334-354/Domain: transmembrane #status predicted <TM1>  
F:378-401/Domain: transmembrane #status predicted <TM2>  
F:419-436/Domain: transmembrane #status predicted <TM3>  
F:457-471/Domain: transmembrane #status predicted <TM4>  
F:504-527/Domain: transmembrane #status predicted <TM5>  
F:612-630/Domain: transmembrane #status predicted <TM6>  
F:636-661/Domain: transmembrane #status predicted <TM7>

Query Match 4.8%; Score 190.5; DB 2; Length 1275;  
Best Local Similarity 19.9%; Pred. No. 3.1e-06;  
Matches 130; Conservative 98; Mismatches 253; Indels 171; Gaps 27;  
QY 153 NAOCTDDYRGHSALHIAIEKRSLOCVKLLVNGANVHARACGRFFQKGCTCFYFGEPL 212  
DB 62 NINCTDPNMR--SALISAENENFDMVILLENHIEV-----GDALLHAISEY 108  
QY 213 LSLAACKQWDVSVYLLNPHOPASLOATDSQNTV---LHLMVMSNSAENIALVTS 269  
DB 109 VEAVEBELLOWEETNH---KEGQPSWEAVDRSKSTFTVDITPLILAAHRNNYILKI---- 162  
QY 270 YDGLLOAGARL-----CPTVQLED-----IRNLQDLTPLKLAKEG 306  
DB 163 ----LLDRGATLPMHDVKCGDCVTSQTDSLRHSQSRINAYRALSASSIALSSRPV 219  
QY 307 IBIFRHILQREFSGLSHRKFTWCYGPVRVSLYDLAS--VDSCEENSVLBIIFPHCKS 364  
DB 220 LTAFO--LSWELKRLQAMESEFRAE-YTEMQMVQDFGTSLLDHARTSMELEVMNFH 276  
QY 365 P-----HRRMVVLEP-LNKLLQAKWDLIPKE----- 391  
DB 277 PSHDIWCLGQRTLERLKLAIKYKQTFVAHPNVQQLAAIWDGLPGFRRKQASQQLMD 336  
QY 392 FLNFCNLNLYMFIFTAVAVHPTLKKQAAPHLKAEVGNMMLTGHILILLGGIYLLVGOL 451  
DB 337 VVKLGCSFPYIISKYLAPDSEGAKFMRKPFVKPFIHSCSYM--PFLMLLGAASLRVQI 394  
QY 452 -----WYF-----WRRH-----VF-----I 461  
DB 395 TPELLAPPWMLTMDWRKHERGSLPGPIELAIITVIMALIPEELKSLYSDGLFEYIMDL 454  
QY 462 W--ISPIDSYFELFLP--QALLTVVSQVLCFLAIEWYL-----PLIYS-----A 502  
DB 455 MNVIDYISNMFYVTILCRATAWVIVHRDLWFRGIDPYFPREHWHFDPMLLSGFAAG 514  
QY 503 LVGLMNLNLYYTRGFQHTGIYSVMIOKVILRDLRLFLLYLVFLGFVALVLSQEAQR 562  
DB 515 MVFSYKLVHIFINPHLGPLQVSLGRMII-DIIKFFIYTLVLFAG--CGLNQLLWY 570  
QY 563 PEAPTGNATESVQPMGEDEGNGA-----QYRGILEASLELFKFTIGMELAFQ--- 614  
DB 571 -YAELEKNKCYHLHPDVADFDQEKACTIWRREFSNLFQSLFWSFGLVLDVSPDLG 629  
QY 615 -QLHFRGMVLLLLAYVLLTYILLNMLIAMSSETVNSVATDSWSIWKLQKA 665  
DB 630 IKSFTRFWALLMFGYSVINIIVLLNMLIAMNSYQIISERADTEWKFA 681

RESULT 15  
I38361  
TRPC1 protein - human  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 04-Sep-1998  
C:Accession: I38361  
R:Wes, P.D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.  
Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995  
A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.  
A:Reference number: I38361; MUID:96003837; PMID:7568191  
A:Accession: I38361  
A>Status: preliminary; translated from GB/EMBL/DBJ



A:Molecule type: mRNA  
A:Residues: 1-810 <RES>  
A:Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787  
C:Superfamily: TRPC3 protein

Query Match 4.3%; Score 174; DB 2; Length 810;  
Best Local Similarity 19.1%; Pred. No. 3.3e-05;  
Matches 139; Conservative 116; Mismatches 244; Indels 228; Gaps 33;

Qy	86	GVPEDLAAGLPEY-----LQTSKYLTDEYTEGSTGKTCMKAV-----	124
Db	37	GAPPPSPGLPPSWAAMAAALYPSDLSGASSSLSPSPSSSPNEVMALADREVKEENT	96
Qy	125	LNLLKQGVNAC-----ILPLQIDRDGPNPQPLVNAQCTDDVYRGHSALHIAIEKRSIQ	177
Db	97	LNKKLFLACDKGYNVKKILE-ENSSGD-----LNINCVD--VLGRNAVITYIENELD	149
Qy	178	CVKLLVNGANVHARACGRFFQKQGTCTF--YFGEPLSLAACTKQMDVVVSYLE-----	230
Db	150	ILQLLLDYG-----CQKLWERIQNPEYSTTMDVAPVILAHRNNYIEIITMLLKQDVSL	202
Qy	231	-NPH-----OPASLOATDSQGNVTVLHALVMISD	257
Db	203	PKPHAVGCECTCSAKNKDSLRSRPRLDIYRCLASPALIMLTEE--DPILRAFELSAD	260
Qy	258	-----NSAENIALVTSMYDGLLOAGARLCTVQLEDIRN-----	291
Db	261	LKELSLVEFRNDYEBELARQCKMFADLLAQAR--NSRELEVILNHTSSDEPLDKRGLL	318
Qy	292	--LQDLTPLKAAKEGKIEIPRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDS	349
Db	319	EERNVLSRLKLAIKYN-----QKEF-----VSQSNC	344
Qy	350	EENSVLEIIAPHCKSPHRR-----MVVLE-----PINKLL-----QAKWDLILPKFFL	393
Db	345	QO--FLNTVWFQMGSGYRRKPTCKIMTVLTGIFWFPVLSLCYLIAPKSQFGRIITPFM	402
Qy	394	NFLCNLIYMFIFT-----AVAYHPTLKQAAAPHLKAEVGNMLLTGHILILGGIYLL	447
Db	403	KPIIHGASYFTFLLLNLVSLVYNEDK-----KNTWGPALERIDYLLIL-----WI	448
Qy	448	VGQLWYFWRHRHFIWIFIDSYPE-----ILFLPQA--LLTVVSQVLCFLAI-----E	493
Db	449	IGMIWSDIKR---LWYEGLEDPLEESRNQLSFVNLSYLATFALKVVAHNKFDHFDARKD	505
Qy	494	W--YLPPLVLSALVGLWNLNLYYTRGFOHTGIYSVM-----IQKVILRDLRLFLIYLVFL	546
Db	506	WDAFHPTLVAGLFAFANVLSYLRFLFFMYTTSSILGPLQISMGOMLQDFGKFLGMFLVL	565
Qy	547	EGPAVALVLSQBAWRPEAPTGNATESVQPMGEQDEGNGCAQYRGILEASLELFKFTIG	606
Db	566	FSFTIGLTQLYDKGY-----TSKQKQCVGIFCQSQNDT---FHSFTGTCFALFWYIFS	617
Qy	607	MGELAF-----QEQLHFRGMVLLILILAYVLLTYILLNMLIAMSSETVNSVATDSWS	658
Db	618	LAHVAIFVTRSYSGEELQSFVGA--IVGTNNVVVIVITKLLVAMLHKSFQLIANHEDK	675
Qy	659	IWKLQKA 665	
Db	676	EWKFARA 682	

Search completed: October 5, 2005, 11:24:15  
Job time : 24 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 5, 2005, 11:12:14 ; Search time 165 Seconds  
(without alignments)  
1790.818 Million cell updates/sec

Title: US-09-445-614B-2  
Perfect score: 4004.  
Sequence: 1 MTPSSSPVRLTLGGQE.....EEDGASENYPVQLQSN 764

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Result No.	Score	Query Match	Length	ID	Description
1	4004	100.0	764	2 AAY29469	Human van
2	4004	100.0	764	2 AAY06559	Human van
3	4004	100.0	764	3 AAY97358	Human VR-
4	4004	100.0	764	4 AAB35622	Human van
5	4004	100.0	764	5 AAM51859	Human van
6	4004	100.0	764	5 ABB07817	Human van
7	4004	100.0	764	6 ABB04099	Human exp
8	4004	100.0	764	6 ABU04113	Human exp
9	4004	100.0	764	6 ABU04095	Human exp
10	4004	100.0	764	6 ABU04104	Human exp
11	4004	100.0	764	6 ABU04110	Human exp
12	4004	100.0	764	6 ABU04106	Human exp
13	4004	100.0	764	6 ABU04096	Human exp
14	4004	100.0	764	8 ADI81598	Human van
15	4004	100.0	764	8 ADP66663	Human van
16	4004	100.0	764	8 ADQ89074	Human uro
17	4004	100.0	764	8 ADP25061	PRO polyp
18	3998	99.9	764	4 AAE04890	Human tra
19	3998	99.9	764	4 ABE01230	Human van
20	3998	99.9	764	6 ABU04101	Human exp
21	3998	99.9	764	6 ABU04100	Human exp
22	3988.5	99.6	763	2 AAY29471	Human van
23	3988.5	99.6	763	2 AAY42308	Human van
24	3988.5	99.6	763	6 ABU04107	Human exp
25	3988.5	99.6	763	6 ABU04098	Human exp

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4004	100.0	764	2 AAY29469	Human van
2	4004	100.0	764	2 AAY06559	Human van
3	4004	100.0	764	3 AAY97358	Human VR-
4	4004	100.0	764	4 AAB35622	Human van
5	4004	100.0	764	5 AAM51859	Human van
6	4004	100.0	764	5 ABB07817	Human van
7	4004	100.0	764	6 ABB04099	Human exp
8	4004	100.0	764	6 ABU04113	Human exp
9	4004	100.0	764	6 ABU04095	Human exp
10	4004	100.0	764	6 ABU04104	Human exp
11	4004	100.0	764	6 ABU04110	Human exp
12	4004	100.0	764	6 ABU04106	Human exp
13	4004	100.0	764	6 ABU04096	Human exp
14	4004	100.0	764	8 ADI81598	Human van
15	4004	100.0	764	8 ADP66663	Human van
16	4004	100.0	764	8 ADQ89074	Human uro
17	4004	100.0	764	8 ADP25061	PRO polyp
18	3998	99.9	764	4 AAE04890	Human tra
19	3998	99.9	764	4 ABE01230	Human van
20	3998	99.9	764	6 ABU04101	Human exp
21	3998	99.9	764	6 ABU04100	Human exp
22	3988.5	99.6	763	2 AAY29471	Human van
23	3988.5	99.6	763	2 AAY42308	Human van
24	3988.5	99.6	763	6 ABU04107	Human exp
25	3988.5	99.6	763	6 ABU04098	Human exp

ALIGNMENTS

RESULT 1  
AAY29469  
ID AAY29469 standard; protein; 764 AA.  
XX  
AC AAY29469;  
XX  
DT 08-OCT-1999 (first entry)  
XX  
DE Human vanilloid receptor homologue VANILREP2.  
XX  
KW Human; vanilloid receptor homologue; VANILREP2; polymorphic variant; PVP-1; therapy; diagnosis; chronic pain; neuropathic; postoperative; rheumatoid arthritis; neuralgia; algesia; nerve injury; ischaemia; neurodegeneration; stroke; incontinence; inflammatory disorder.  
XX  
OS Homo sapiens.  
XX  
FN WO9937765-A1.  
XX  
PD 29-JUL-1999.  
XX  
PF 25-JAN-1999; 99WO-EP000420.  
XX  
PR 27-JAN-1998; 98EP-00300549.  
PR 26-OCT-1998; 98GB-00023421.  
PR 20-JAN-1999; 99GB-00001209.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Davis JB, Duckworth DM, Hayes PD;  
XX  
DR WPI: 1999-479049/40.  
XX  
DR N-PSDB; AAZ07114.  
XX  
PS New human vanilloid receptor homologues (VANILREP2).  
XX  
CC Claim 4; Page 30-32; 47pp; English.  
XX  
CC The present sequence represents a human vanilloid receptor homologue, designated VANILREP2. VANILREP2 can be used to diagnose disease or susceptibility to disease related to expression or activity of VANILREP2 polypeptides. VANILREP2 may be used to treat diseases including pain, (for example chronic, neuropathic, postoperative, rheumatoid arthritis), neuralgia, algesia, nerve injury, ischaemia, neurodegeneration, stroke, incontinence, and inflammatory disorders  
XX  
SQ Sequence 764 AA;

26	3988.5	99.6	763	6	ABU04108	Human exp
27	3988.5	99.6	889	5	ABG99067	Human van
28	3988.5	99.6	889	6	ABO42807	Human van
29	3945	98.5	764	5	AAM51860	Human van
30	3945	98.5	764	5	ABB07818	Human van
31	3945	98.5	764	6	ABU04112	Human exp
32	3945	98.5	764	6	ABU04097	Human exp
33	3945	98.5	764	6	ABU04114	Human exp
34	3945	98.5	764	8	ADI81600	Human van
35	3945	98.5	764	8	ADP09701	Human VRL
36	3939	98.4	764	3	AAY84834	Amino aci
37	3939	98.4	764	6	ABU04109	Human exp
38	3375	84.3	644	8	ADI81574	Human van
39	3258	81.4	630	3	AAY97364	Human VR-
40	3258	81.4	630	6	ABU04111	Human exp
41	3159	78.9	756	8	ADI81616	Mouse gro
42	3158	78.9	756	8	ADI81582	Mouse van
43	3051.5	76.2	761	2	AAY06556	Rat vanil
44	3051.5	76.2	761	2	AAY99790	Rat VRRP-
45	3051.5	76.2	761	8	ADI81576	Rat vanil

Query Match	100.0%;	Score 4004;	DB 2;	Length 764;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 764;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	MTSPSSPVRLTLDGGQDGEADRGKLDGSGLPPMESQFGEDRKFAFQIRVNLNY	60		
Db	1	MTSPSSPVRLTLDGGQDGEADRGKLDGSGLPPMESQFGEDRKFAFQIRVNLNY	60		
QY	61	RKGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKYLTDSEYTGSTGKTCL	120		
Db	61	RKGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKYLTDSEYTGSTGKTCL	120		
QY	121	MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSIQCVK	180		
Db	121	MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSIQCVK	180		
QY	181	LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQWDVSYLLENPHQPASLOA	240		
Db	181	LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQWDVSYLLENPHQPASLOA	240		
QY	241	TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPLKL	300		
Db	241	TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPLKL	300		
QY	301	AAKEGKIEIFRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF	360		
Db	301	AAKEGKIEIFRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF	360		
QY	361	HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAVAYHOPTLKKQAA	420		
Db	361	HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAVAYHOPTLKKQAA	420		
QY	421	PHLKAEGVNSMLTGHILLLGGIYLLVQGLWYFWRHVFIMISFIDSYPEILFLFOALL	480		
Db	421	PHLKAEGVNSMLTGHILLLGGIYLLVQGLWYFWRHVFIMISFIDSYPEILFLFOALL	480		
QY	481	TVVSQVLCFLAIEWYLPPLVLSALVGLWNLVYTRGFQHTGIYSVMIQVILRDILRFL	540		
Db	481	TVVSQVLCFLAIEWYLPPLVLSALVGLWNLVYTRGFQHTGIYSVMIQVILRDILRFL	540		
QY	541	IYLVFLFGFAVALVLSQEAWRPEAPTGNPNATESVQMEGQDEGNGAQRGILEASLEL	600		
Db	541	IYLVFLFGFAVALVLSQEAWRPEAPTGNPNATESVQMEGQDEGNGAQRGILEASLEL	600		
QY	601	FKFTIGMGLAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW	660		
Db	601	FKFTIGMGLAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW	660		
QY	661	KLOKALSIVLEMENGYWCRKKQAGVMLTVGTPDGSPOBERWCFRVEEYNWASWEQTLPT	720		
Db	661	KLOKALSIVLEMENGYWCRKKQAGVMLTVGTPDGSPOBERWCFRVEEYNWASWEQTLPT	720		
QY	721	LCBDPSGAGVPTLENPVLASPPKDEDDGASEENYVPVQLQSN 764			
Db	721	LCBDPSGAGVPTLENPVLASPPKDEDDGASEENYVPVQLQSN 764			

RESULT 2  
AAY06559  
ID AAY06559 standard; protein; 764 AA.  
XX  
AC AAY06559;  
XX  
XX  
DT 08-OCT-1999 (first entry)  
XX  
DE Human vanilloid receptor-related polypeptide 1 (VRRP-1).  
XX  
KW Vanilloid receptor-related polypeptide 1; VRRP-1; VR2;  
KW capsaicin receptor; VR1; human; vanilloid; analgesic; pain; inflammation;  
XX therapy; diagnosis.  
XX  
OS Homo sapiens.  
XX

PN	W09937675-A1.				
XX					
PD	29-JUL-1999.				
XX					
PF	22-JAN-1999; 99WO-US001418.				
XX					
PR	22-JAN-1998; 98US-0072151P.				
XX					
PA	(REGC ) UNIV CALIFORNIA.				
XX					
PI	Julius DJ, Caterina M, Brake AJ;				
XX					
DR	WPI; 1999-469113/39.				
XX	N-PSDB; AAX87492.				
DR					
PT	New isolated capsaicin receptor polypeptide and related nucleic acid -				
PT	useful for detecting vanilloid compounds, identifying modulators, and in				
PT	diagnosis or treatment of e.g. pain and inflammation.				
XX					
PS	Claim 4; Page 110-112; 120pp; English.				
XX					
CC	The present sequence represents human vanilloid receptor-related				
CC	polypeptide 1 (VRRP-1 or VR2), as deduced from a cDNA clone (see				
CC	AAX87492) isolated from human CCRF-CEM cells. VRRP-1 is an example of a				
CC	capsaicin receptor-related polypeptide of the invention. It is not				
CC	activated by capsaicin or heat, but may interact with the novel capsaicin				
CC	receptor VR1 (see AAY06558). The invention provides vanilloid receptor				
CC	polypeptides and polynucleotides, including capsaicin receptor-related				
CC	polypeptides and polynucleotides, as well as expression vectors, host				
CC	cells and transgenic animals. It also provides a method of using such				
CC	receptors to identify vanilloid compounds in natural products or to				
CC	screen candidate compounds that modulate capsaicin receptor function for				
CC	use as analgesics (vanilloid analogues, therapeutic antibodies, antisense				
CC	oligonucleotides, capsaicin receptor-encoding polynucleotides for gene				
CC	therapy), flavour-enhancing agents, etc. Capsaicin receptor-related				
CC	polypeptides and specific antibodies can also be used for the diagnosis				
CC	and treatment of human disease and pain				
XX					
SQ	Sequence 764 AA;				
Query Match	100.0%;	Score 4004;	DB 2;	Length 764;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 764;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	MTSPSSPVRLTLDGGQDGEADRGKLDGSGLPPMESQFGEDRKFAFQIRVNLNY	60		
Db	1	MTSPSSPVRLTLDGGQDGEADRGKLDGSGLPPMESQFGEDRKFAFQIRVNLNY	60		
QY	61	RKGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKYLTDSEYTGSTGKTCL	120		
Db	61	RKGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKYLTDSEYTGSTGKTCL	120		
QY	121	MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSIQCVK	180		
Db	121	MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSIQCVK	180		
QY	181	LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQWDVSYLLENPHQPASLOA	240		
Db	181	LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQWDVSYLLENPHQPASLOA	240		
QY	241	TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPLKL	300		
Db	241	TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPLKL	300		
QY	301	AAKEGKIEIFRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF	360		
Db	301	AAKEGKIEIFRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF	360		
QY	361	HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAVAYHOPTLKKQAA	420		
Db	361	HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAVAYHOPTLKKQAA	420		
QY	421	PHLKAEGVNSMLTGHILLLGGIYLLVQGLWYFWRHVFIMISFIDSYPEILFLFOALL	480		

FT	Modified-site	604..607	/label= transmembrane_domain
FT	Domain	621..645	/note= "N-glycosylation site"
FT	Modified-site	622..628	/label= transmembrane_domain
FT	Modified-site	749..752	/note= "tyrosine kinase phosphorylation site"
FT	Modified-site	765..770	/note= "N-glycosylation site"
FT	Modified-site		/note= "myristoylation site"
XX		WO200029577-1.	
PN		25-MAY-2000.	
PD		12-NOV-1999;	99WO-US026701.
XX		13-NOV-1998;	98US-0108322P.
PR		28-DEC-1998;	98US-0114078P.
PR		26-FEB-1999;	99US-00258633.
PR		19-OCT-1999;	99US-00421134.
XX		(MILL-) MILLENNIUM PHARM INC.	
XX		Curtis RAJ;	
XX		WPI; 2000-387790/33.	
DR		N-PSDB; AAA30254.	
XX		New capsaicin/vanilloid receptor polynucleotides and polypeptides, used to modulate pain signaling mechanisms.	
PT		Claim 11; Fig 2; 183pp; English.	
XX		The present sequence is the protein sequence for human capsaicin/vanilloid receptor VR-2, which is involved in pain signalling. The coding sequence was isolated by searching a heart cDNA library for genes encoding novel receptors of the capsaicin/vanilloid family, and has been shown to be located at chromosome 17p11-12. This region has been associated with myasthenia gravis, Smith-Magenis syndrome, CORDS, Congenital rod dystrophy, choroidal dystrophy, central areolar and retinal cone dystrophy, and it is possible that the protein may be used to treat or diagnose these disorders. In addition, the gene, protein and its antibodies can be used to diagnose and treat hyperalgesia, inflammation, infection, ischaemia, joint pain, tooth pain, headaches, pain associated with surgery or neuropathic pain, possibly via the use of gene therapy	
XX		Sequence 764 AA;	
Qy		Query Match 100.0%; Score 4004; DB 3; Length 764;	
Db		Best Local Similarity 100.0%; Pred. No. 0;	
Db		Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MTSPSSSPVFRLETLDGQGDSEADRGKLDGSGLPMPMESQFGEDRKFPQIRVNLNY	60
Db	1	MTSPSSSPVFRLETLDGQGDSEADRGKLDGSGLPMPMESQFGEDRKFPQIRVNLNY	60
Qy	61	RKGTGASQDPNPRFDRDLFNVAISRGVPEDLAGLPEYLSKYLTDSEYTGSTGKTCL	120
Db	61	RKGTGASQDPNPRFDRDLFNVAISRGVPEDLAGLPEYLSKYLTDSEYTGSTGKTCL	120
Qy	121	MKAVNLKQGVNACILPLQLIQRDSDGNPQPLVNAQCTDDYRHSALHIAIEKESLQCVK	180
Db	121	MKAVNLKQGVNACILPLQLIQRDSDGNPQPLVNAQCTDDYRHSALHIAIEKESLQCVK	180
Qy	181	LLVENGANVHARACGRFFQKQGCTCFYFGLPLSLAACTKQMDVSVSYLLENPHQPASLOA	240
Db	181	LLVENGANVHARACGRFFQKQGCTCFYFGLPLSLAACTKQMDVSVSYLLENPHQPASLOA	240
Qy	241	TDSQGNVTLHALVMSIDNSAENIALVTSMDGLLQAGARLCPTVQLEDIRNLODLTPKL	300
Db	241	TDSQGNVTLHALVMSIDNSAENIALVTSMDGLLQAGARLCPTVQLEDIRNLODLTPKL	300

QY 301 AAKEGKIEIFRHILOREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAP 360  
DB 301 AAKEGKIEIFRHILOREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAP 360  
QY 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKFPLNLCNLIYMFIFTAVAYHPTLKKQAA 420  
DB 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKFPLNLCNLIYMFIFTAVAYHPTLKKQAA 420  
QY 421 PHLKAEVGNMMLTGHLILGGLYLLVQWLMYFMRHVFIIWISFIDSIFEILFLFQALL 480  
DB 421 PHLKAEVGNMMLTGHLILGGLYLLVQWLMYFMRHVFIIWISFIDSIFEILFLFQALL 480  
QY 481 TVVSQVLCFLAIEWYLPLLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRDLRFL 540  
DB 481 TVVSQVLCFLAIEWYLPLLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRDLRFL 540  
QY 541 IYLVFLFGFAVALVSLSQEAWRPEAPTPGNATESVQPMGEQDEGNGAQRGILEASLEL 600  
DB 541 IYLVFLFGFAVALVSLSQEAWRPEAPTPGNATESVQPMGEQDEGNGAQRGILEASLEL 600  
QY 601 FKFTIGMGLAFQEQHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
DB 601 FKFTIGMGLAFQEQHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
QY 661 KLOKAISVLEMENGYWCRKKQKQAGVMLTVGTYPDGSPPDERWCPRVEEVNWNASWEOTLPT 720  
DB 661 KLOKAISVLEMENGYWCRKKQKQAGVMLTVGTYPDGSPPDERWCPRVEEVNWNASWEOTLPT 720  
QY 721 LCEDPSGAGVPRTPLENPVLASPPKDEDDGASEENYVPVQLQSN 764  
DB 721 LCEDPSGAGVPRTPLENPVLASPPKDEDDGASEENYVPVQLQSN 764

RESULT 4  
AAB35622  
ID AAB35622 standard; protein; 764 AA.  
XX AAB35622;  
DT 14-FEB-2001 (first entry)  
XX Human vanilloid receptor like receptor protein.  
DE  
XX VR-L; vanilloid receptor-like receptor; pain; infection; allergy;  
KW mechanical injury; lymphoid tissue; human.  
XX Homo sapiens.  
XX GB2346882-A.  
XX 23-AUG-2000.  
XX 02-DEC-1999; 99GB-00028566.  
XX 08-DEC-1998; 98GB-00027016.  
XX (MERI ) MERCK SHARP & DOHME LTD.  
PA Bonnert TP;  
PI  
XX WPI; 2001-064250/08.  
DR N-PSDB; AAC60297.  
XX New polynucleotide encoding human vanilloid receptor-like receptor for  
PT diagnosing and treating pain, infections, allergies, and cancers.  
XX Claim 1; Fig 1; 36pp; English.  
XX The present invention relates to the human vanilloid receptor-like  
CC receptor. This receptor may be used for diagnosing or treating conditions  
CC associated with altered vanilloid receptor-like (VR-L) receptor  
CC expression. It may also be used to treat abnormal conditions associated

CC with pain. Conditions or diseases that can be diagnosed or treated  
CC include viral, bacterial and fungal infections, allergic responses,  
CC mechanical injury associated with trauma, hereditary diseases, lymphoma  
CC or carcinoma, or other conditions which activate the genes of the  
CC lymphoid tissues  
XX  
SQ Sequence 764 AA;  
Query Match 100.0%; Score 4004; DB 4; Length 764;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTSPPSSPVRLETLDGGQDGEADRGKLDGSGLPWMEQFQGEDRKFAFQIRVNLNY 60  
DB 1 MTSPPSSPVRLETLDGGQDGEADRGKLDGSGLPWMEQFQGEDRKFAFQIRVNLNY 60  
QY 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTESGKTCL 120  
DB 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTESGKTCL 120  
QY 121 MKAVNLKDGVNACILPLLIQIDRDSGNPOPLVNAOCTDDYRGHSAHIAIEKRSIQCVK 180  
DB 121 MKAVNLKDGVNACILPLLIQIDRDSGNPOPLVNAOCTDDYRGHSAHIAIEKRSIQCVK 180  
QY 181 LLVENGANVHABACGRFFQKGGCTCFYFGEPLSLAACTKQWDVSYLLENPHQASLOA 240  
DB 181 LLVENGANVHABACGRFFQKGGCTCFYFGEPLSLAACTKQWDVSYLLENPHQASLOA 240  
QY 241 TDSQNTVHLHALVMTSDNSAENIALVTSMYDGLQAGARLCPTVQLEDIRNLQDLTPLKL 300  
DB 241 TDSQNTVHLHALVMTSDNSAENIALVTSMYDGLQAGARLCPTVQLEDIRNLQDLTPLKL 300  
QY 301 AAKEGKIEIFRHILOREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAP 360  
DB 301 AAKEGKIEIFRHILOREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAP 360  
QY 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKFPLNLCNLIYMFIFTAVAYHPTLKKQAA 420  
DB 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKFPLNLCNLIYMFIFTAVAYHPTLKKQAA 420  
QY 421 PHLKAEVGNMMLTGHLILGGLYLLVQWLMYFMRHVFIIWISFIDSIFEILFLFQALL 480  
DB 421 PHLKAEVGNMMLTGHLILGGLYLLVQWLMYFMRHVFIIWISFIDSIFEILFLFQALL 480  
QY 481 TVVSQVLCFLAIEWYLPLLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRDLRFL 540  
DB 481 TVVSQVLCFLAIEWYLPLLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRDLRFL 540  
QY 541 IYLVFLFGFAVALVSLSQEAWRPEAPTPGNATESVQPMGEQDEGNGAQRGILEASLEL 600  
DB 541 IYLVFLFGFAVALVSLSQEAWRPEAPTPGNATESVQPMGEQDEGNGAQRGILEASLEL 600  
QY 601 FKFTIGMGLAFQEQHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
DB 601 FKFTIGMGLAFQEQHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
QY 661 KLOKAISVLEMENGYWCRKKQKQAGVMLTVGTYPDGSPPDERWCPRVEEVNWNASWEOTLPT 720  
DB 661 KLOKAISVLEMENGYWCRKKQKQAGVMLTVGTYPDGSPPDERWCPRVEEVNWNASWEOTLPT 720  
QY 721 LCEDPSGAGVPRTPLENPVLASPPKDEDDGASEENYVPVQLQSN 764  
DB 721 LCEDPSGAGVPRTPLENPVLASPPKDEDDGASEENYVPVQLQSN 764  
RESULT 5  
AAM51859  
ID AAM51859 standard; protein; 764 AA.  
XX AAM51859;  
AC AAM51859;  
XX 29-JAN-2002 (first entry)  
XX

DE Human vanilloid receptor 1.  
 XX Human; TLCC-2; TRP-like calcium channel; membrane excitability;  
 KW nociception; nootropic; neuroprotective; antiparkinsonian; cytostatic;  
 KW hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser;  
 KW Parkinson's disease; Huntington's disease; multiple sclerosis;  
 KW Gilles de la Tourette's syndrome; autonomic function disorder; cancer;  
 KW neuroleptic; gene therapy; Alzheimer's disease; CNS disorder.  
 XX Homo sapiens.  
 OS W0200177331-A1.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-US011442.  
 XX 07-APR-2000; 2000US-00544797.  
 XX (MILL-) MILLENITUM PHARM INC.  
 XX Curtis RAJ, Silos-Santiago I;  
 XX WPI; 2002-010913/01.  
 XX Novel isolated human transient receptor potential-like calcium channel  
 PT protein-2 useful for treating Alzheimer's disease, depression, amnesia,  
 PT pain disorder, and cancer.  
 XX Example 1; Page 131-134; 148pp; English.  
 XX The present invention relates to the protein and coding sequences of  
 CC human transient receptor potential (TRP)-like calcium channel protein-2  
 CC (TLCC-2). The sequences can be used in the treatment of TLCC-2 related  
 CC disorders, including central nervous system disorders such as  
 CC Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis,  
 CC Gilles de la Tourette's syndrome, autonomic function disorders, learning  
 CC or memory disorders, pain disorders and disorders of cellular  
 CC proliferation, including cancer. The present sequence is the human  
 CC vanilloid receptor 1 which was described in the exemplification of the  
 CC invention  
 XX Sequence 764 AA;  
 SQ  
 Query Match 100.0%; Score 4004; DB 5; Length 764;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTPSSSPVFRLETLDDGGQDSEADRGKLDGSGLPPEMESQFQGEDRKEAPQIRVNLNY 60  
 DB 1 MTPSSSPVFRLETLDDGGQDSEADRGKLDGSGLPPEMESQFQGEDRKEAPQIRVNLNY 60  
 QY 61 RKGTGASQPDNRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSYEGSTGKTCL 120  
 DB 61 RKGTGASQPDNRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSYEGSTGKTCL 120  
 QY 121 MKAVLNLDKGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRHSALHIAIEKRSLOCVK 180  
 DB 121 MKAVLNLDKGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRHSALHIAIEKRSLOCVK 180  
 QY 181 LLVENGANVHARACGRPFQKQGGTCFYFGEPLSLAACTKQDWVSVYLLNPHOPASLOA 240  
 DB 181 LLVENGANVHARACGRPFQKQGGTCFYFGEPLSLAACTKQDWVSVYLLNPHOPASLOA 240  
 QY 241 TDSQNTVHLVMISSNSAENIALVTSMYDGLLQAGARLCTTVQLEDIRNLQDLTLPKL 300  
 DB 241 TDSQNTVHLVMISSNSAENIALVTSMYDGLLQAGARLCTTVQLEDIRNLQDLTLPKL 300  
 QY 301 AAKEGKIEIFRHILQREFSGLSLSRKFTWCYGPVRVSLYDLASVDSCEANSVLEIAP 360  
 DB 301 AAKEGKIEIFRHILQREFSGLSLSRKFTWCYGPVRVSLYDLASVDSCEANSVLEIAP 360  
 QY 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKFFLNFLCNLIYFIPTAVAHQPTLKKQAA 420

DB 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKFFLNFLCNLIYFIPTAVAHQPTLKKQAA 420  
 QY 421 PHLKAEGVNSMLTGHILGIIYLLGQWYFRRHVFIWISFIDSFYFELFLFOALL 480  
 DB 421 PHLKAEGVNSMLTGHILGIIYLLGQWYFRRHVFIWISFIDSFYFELFLFOALL 480  
 QY 481 TVVSQVLCFLALEWYLLPLVLSALVGLWNLMLLYTRGFQHTGIYSVMQKVIIRDLLRFL 540  
 DB 481 TVVSQVLCFLALEWYLLPLVLSALVGLWNLMLLYTRGFQHTGIYSVMQKVIIRDLLRFL 540  
 QY 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMEGQDEGNGAQYRGLEASLEL 600  
 DB 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMEGQDEGNGAQYRGLEASLEL 600  
 QY 601 FKFTTGMGELAFQEQHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660  
 DB 601 FKFTTGMGELAFQEQHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660  
 QY 661 KLQKAI SVLEMENGYWCRKQKQAGVMTVGTGPDGSPDERMCFRVEEVNWSWEQTLPT 720  
 DB 661 KLQKAI SVLEMENGYWCRKQKQAGVMTVGTGPDGSPDERMCFRVEEVNWSWEQTLPT 720  
 QY 721 LCEDPSGAGVPRTELENVPLASPPKEDDGCASENYPVQLQSN 764  
 DB 721 LCEDPSGAGVPRTELENVPLASPPKEDDGCASENYPVQLQSN 764  
 RESULT 6  
 ABB07817  
 ID ABB07817 standard; protein; 764 AA.  
 XX ABB07817;  
 AC ABB07817;  
 DT 03-JUL-2002 (first entry)  
 XX Human vanilloid receptor 1.  
 KW Transient receptor potential like calcium channel; TRP; TLCC-2; human;  
 KW neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant;  
 KW cerebroprotective; anxiolytic; antimanic; anticonvulsant; gene therapy;  
 KW calcium signaling; vanilloid receptor 1.  
 XX Homo sapiens.  
 XX US2002035056-A1.  
 XX 21-MAR-2002.  
 XX 06-APR-2001; 2001US-00828466.  
 XX 07-APR-2000; 2000US-00544797.  
 XX (CURT/) CURTIS R A J.  
 XX (SILO/) SILOS-SANTIAGO I.  
 XX Curtis RAJ, Silos-Santiago I;  
 XX WPI; 2002-338931/37.  
 XX New nucleic acid designated TLCC-2 encodes a transient receptor potential  
 PT -like calcium channel and is useful to diagnose and treat pain disorders  
 PT and central nervous system neurodegenerative and neurological disorders.  
 XX Disclosure; Fig 6; 70pp; English.  
 XX The invention relates to a novel transient receptor potential (TRP)-like  
 CC calcium channel, designated TLCC-2 and polynucleotides encoding the TLCC-  
 CC 2. TLCC-2 can be expressed by standard recombinant methodology. The TLCC-  
 CC 2 polypeptide, polynucleotides and modulators are useful for treating  
 CC central nervous system disorders such as neurodegenerative disorders for  
 CC example Alzheimer's disease, Parkinson's disease, multiple sclerosis,  
 CC amyotrophic lateral sclerosis, progressive supranuclear palsy, epilepsy,



CC Creutzfeldt-Jakob disease, AIDS-related dementia, familial infantile  
CC convulsions, paroxysmal choreoathetosis, psychiatric disorders such as  
CC depression, anxiety, schizophrenia, psychosis, mania or phobic disorders,  
CC learning or memory disorders such as amnesia, age-related memory loss, or  
CC a neurological disorder such as migraine. The molecules are also useful  
CC to treat a pain disorder. The present sequence represents a human  
CC vanilloid receptor 1, used in alignment studies with the rVLC-2  
CC polypeptide  
XX  
SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 5; Length 764;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSPVFRLETLDDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFAFQIRVNLNY 60  
DB 1 MTSPPSPVFRLETLDDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFAFQIRVNLNY 60  
QY 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTGSTGKTCL 120  
DB 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTGSTGKTCL 120  
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRSHSALHIAIEKRSIQCVK 180  
DB 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRSHSALHIAIEKRSIQCVK 180  
QY 181 LLVENGANVHARACGRFFQKGGQCTCFYFGBELPLSLAACTQWDVSVYLLNPHQASLOA 240  
DB 181 LLVENGANVHARACGRFFQKGGQCTCFYFGBELPLSLAACTQWDVSVYLLNPHQASLOA 240  
QY 241 TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLLQAGARLCPVQLEDIRNLDLTPKL 300  
DB 241 TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLLQAGARLCPVQLEDIRNLDLTPKL 300  
QY 301 AAKEGKIEIPRHILQREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSVLRIIAP 360  
DB 301 AAKEGKIEIPRHILQREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSVLRIIAP 360  
QY 361 HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNLCLNIYMFIFTAVAYHPTLKKQAA 420  
DB 361 HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNLCLNIYMFIFTAVAYHPTLKKQAA 420  
QY 421 PHLKAEGVSNMLTGHILILGGIYLLVGQLWTFWRHRHVFIIWISPTDSYFEILFLQALL 480  
DB 421 PHLKAEGVSNMLTGHILILGGIYLLVGQLWTFWRHRHVFIIWISPTDSYFEILFLQALL 480  
QY 481 TVVSQVLCFLAIEWYLPVLSALVGLWNLNLYYTRGFQHTGIYSVMIOKVILRDILRFL 540  
DB 481 TVVSQVLCFLAIEWYLPVLSALVGLWNLNLYYTRGFQHTGIYSVMIOKVILRDILRFL 540  
QY 541 IYLVFLFGFAVALVLSQEAWRPEAPTGPNNATESVQPMQEDGNGAQYRGILEASLEL 600  
DB 541 IYLVFLFGFAVALVLSQEAWRPEAPTGPNNATESVQPMQEDGNGAQYRGILEASLEL 600  
QY 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLYIILLNMLIALMSETVNSVATDSWSIW 660  
DB 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLYIILLNMLIALMSETVNSVATDSWSIW 660  
QY 661 KLOKALSIVLEMENGYWCRKKRAGVNLTVGTRKPDGSPDRWCFRVEEYNWASWEOTLPT 720  
DB 661 KLOKALSIVLEMENGYWCRKKRAGVNLTVGTRKPDGSPDRWCFRVEEYNWASWEOTLPT 720  
QY 721 LCDPDSGAGVPRTLNPVLASPPKDEDDGASEENYVPVQLQSN 764  
DB 721 LCDPDSGAGVPRTLNPVLASPPKDEDDGASEENYVPVQLQSN 764

RESULT 7  
ABU04099  
ID ABU04099  
XX  
AC ABU04099;

XX 29-JAN-2003 (first entry)  
XX Human expressed protein tag (EPT) #765.  
XX Translational profiling; expressed protein tag: EPT; kinase; phosphatase;  
XX protease; protease inhibitor; transporter; cytoskeletal protein;  
XX receptor; transcription factor; cancer; MHC;  
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX Homo sapiens.  
XX WO200278524-A2.  
XX 10-OCT-2002.  
XX 28-MAR-2002; 2002WO-US009671.  
XX 28-MAR-2001; 2001US-0279495P.  
XX 21-MAY-2001; 2001US-0292544P.  
XX 08-AUG-2001; 2001US-0310801P.  
XX 01-OCT-2001; 2001US-0326370P.  
XX 04-DEC-2001; 2001US-0336780P.  
XX 20-FEB-2002; 2002US-0359985P.  
XX (ZYCO-) ZYCO INC.  
XX Chicx RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
XX cytoskeletal proteins, receptors or transcription factors), useful for  
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
XX leukemia.  
XX Example 2; SEQ ID NO 765; 134pp; English.  
XX The invention describes a purified polypeptide, which comprises a  
XX fragment of a kinase, phosphatase, protease, protease inhibitor,  
XX transporter, cytoskeletal protein, receptor or transcription factor. The  
XX polypeptide is useful as an immunogenic composition for eliciting in a  
XX mammal an immunogenic response directed against any of the purified in  
XX polypeptide. The purified polypeptide, or the antibody that binds to this  
XX polypeptide, is useful for treating cancer. The polypeptide is also  
XX useful for identifying compounds that binds to a naturally processed  
XX class I or class II MHC-binding polypeptide. The polypeptides and  
XX polynucleotides are particularly useful for treating or preventing  
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
XX lymphoma or leukaemia. These are also useful for screening agents for  
XX treating the above mentioned diseases. This sequence represents an  
XX expressed protein tag (EPT) isolated from human tissue for translational  
XX profiling. Note: This sequence does not appear in the printed  
XX specification but was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences

Sequence 764 AA;  
Query Match 100.0%; Score 4004; DB 6; Length 764;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTSPPSPVFRLETLDDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFAFQIRVNLNY 60  
DB 1 MTSPPSPVFRLETLDDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFAFQIRVNLNY 60  
QY 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTGSTGKTCL 120  
DB 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTGSTGKTCL 120  
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRSHSALHIAIEKRSIQCVK 180

Db 121 MKAVNLKDGVNACILPLLQIDRDGSGNPQPLVNAQCTDDYRSGHSALHIAIEKRSLQCCKV 180  
 Qy 181 LLVENGANVHARACGRFFQKGCTCFYFGLPLSLAACTKQWDVSVYLLNPHQASLOA 240  
 Db 181 LLVENGANVHARACGRFFQKGCTCFYFGLPLSLAACTKQWDVSVYLLNPHQASLOA 240  
 Qy 241 TDSQGNVTLHALVMSIDNSAENALVTSMYDGLLQAGARLCTVQLEDIRNLQDLTFLKL 300  
 Db 241 TDSQGNVTLHALVMSIDNSAENALVTSMYDGLLQAGARLCTVQLEDIRNLQDLTFLKL 300  
 Qy 301 AAKEGKIEIPRHILQREFSGLSHLRKFTWCYGPVRVSYLDASVDSCEENSVEIIF 360  
 Db 301 AAKEGKIEIPRHILQREFSGLSHLRKFTWCYGPVRVSYLDASVDSCEENSVEIIF 360  
 Qy 361 HCKSPHRRMVLEPLNKLQAKWDLII PKFFLNFLCNLYMFIPTAVAVHQTAKQAA 420  
 Db 361 HCKSPHRRMVLEPLNKLQAKWDLII PKFFLNFLCNLYMFIPTAVAVHQTAKQAA 420  
 Qy 421 PHLKAEGVNSMLLTGHILILGGIYLLVQGLWYFRRHVFIIWISFIDSVEIIFLFOALL 480  
 Db 421 PHLKAEGVNSMLLTGHILILGGIYLLVQGLWYFRRHVFIIWISFIDSVEIIFLFOALL 480  
 Qy 481 TVVSQVLCFLAIEWYLPPLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKILRDLRFL 540  
 Db 481 TVVSQVLCFLAIEWYLPPLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKILRDLRFL 540  
 Qy 541 IYVFLGFAVALVSLQEAWRPEATPGPNATSVQPMQEGDEGNGAQRGILEASLEL 600  
 Db 541 IYVFLGFAVALVSLQEAWRPEATPGPNATSVQPMQEGDEGNGAQRGILEASLEL 600  
 Qy 601 FKFTIGMELAFQSLHFRGMVLLIAYVLLTVLLLNMLIAMSSTVNSVATDSWSIW 660  
 Db 601 FKFTIGMELAFQSLHFRGMVLLIAYVLLTVLLLNMLIAMSSTVNSVATDSWSIW 660  
 Qy 661 KLOKAISVLEMEGYWCRKKQKQAGVMLTVGTGKPDGSPDERWCFRVEEVNWSWEQTLPT 720  
 Db 661 KLOKAISVLEMEGYWCRKKQKQAGVMLTVGTGKPDGSPDERWCFRVEEVNWSWEQTLPT 720  
 Qy 721 LCEPDGAGVPTLENVPLASPPKEDGASEENYVPVQLQSN 764  
 Db 721 LCEPDGAGVPTLENVPLASPPKEDGASEENYVPVQLQSN 764

RESULT 8  
 ABU04113  
 ID ABU04113 standard; protein; 764 AA.  
 AC ABU04113;  
 XX  
 DT 29-JAN-2003 (first entry)  
 DE Human expressed protein tag (EPT) #779.  
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX Homo sapiens.  
 OS  
 FN WO200278524-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 28-MAR-2002; 2002WO-US009671.  
 XX  
 PR 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.  
 PA Chicz RM, Tomlinson AJ, Urban RG;  
 PI WPI; 2003-040607/03.  
 DR  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 XX  
 PS Example 2; SEQ ID NO 779; 134pp; English.  
 XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 764 AA;  
 SQ

Query Match 100.0%; Score 4004; DB 6; Length 764;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSPPSSPVFRLETLTLDGGQDSEADRGKLDGSGLPPEMESQFGEDRKEFAPQIRVNLNY 60  
 Db 1 MTSPPSSPVFRLETLTLDGGQDSEADRGKLDGSGLPPEMESQFGEDRKEFAPQIRVNLNY 60  
 Qy 61 RKGTGASQDPNRFDRDLRFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120  
 Db 61 RKGTGASQDPNRFDRDLRFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120  
 Qy 121 MKAVNLKDGVNACILPLLQIDRDGSGNPQPLVNAQCTDDYRSGHSALHIAIEKRSLQCCKV 180  
 Db 121 MKAVNLKDGVNACILPLLQIDRDGSGNPQPLVNAQCTDDYRSGHSALHIAIEKRSLQCCKV 180  
 Qy 181 LLVENGANVHARACGRFFQKGCTCFYFGLPLSLAACTKQWDVSVYLLNPHQASLOA 240  
 Db 181 LLVENGANVHARACGRFFQKGCTCFYFGLPLSLAACTKQWDVSVYLLNPHQASLOA 240  
 Qy 241 TDSQGNVTLHALVMSIDNSAENALVTSMYDGLLQAGARLCTVQLEDIRNLQDLTFLKL 300  
 Db 241 TDSQGNVTLHALVMSIDNSAENALVTSMYDGLLQAGARLCTVQLEDIRNLQDLTFLKL 300  
 Qy 301 AAKEGKIEIPRHILQREFSGLSHLRKFTWCYGPVRVSYLDASVDSCEENSVEIIF 360  
 Db 301 AAKEGKIEIPRHILQREFSGLSHLRKFTWCYGPVRVSYLDASVDSCEENSVEIIF 360  
 Qy 361 HCKSPHRRMVLEPLNKLQAKWDLII PKFFLNFLCNLYMFIPTAVAVHQTAKQAA 420  
 Db 361 HCKSPHRRMVLEPLNKLQAKWDLII PKFFLNFLCNLYMFIPTAVAVHQTAKQAA 420  
 Qy 421 PHLKAEGVNSMLLTGHILILGGIYLLVQGLWYFRRHVFIIWISFIDSVEIIFLFOALL 480  
 Db 421 PHLKAEGVNSMLLTGHILILGGIYLLVQGLWYFRRHVFIIWISFIDSVEIIFLFOALL 480  
 Qy 481 TVVSQVLCFLAIEWYLPPLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKILRDLRFL 540  
 Db 481 TVVSQVLCFLAIEWYLPPLVLSALVGLWNLIIYTRGFQHTGIYSVMIQKILRDLRFL 540

QY 541 IYLVFPGFAVALVSLQEARPEPTGNATESVQPMQDEGNGAQYRGILEASLEL 600  
Db 541 IYLVFPGFAVALVSLQEARPEPTGNATESVQPMQDEGNGAQYRGILEASLEL 600  
QY 601 FKFTIGMGLAFQELHFRGMVLLLLAYVLLTYILLNNMLIALMSETVNSVATDSWSIW 660  
Db 601 FKFTIGMGLAFQELHFRGMVLLLLAYVLLTYILLNNMLIALMSETVNSVATDSWSIW 660  
QY 661 KLQKAI SVLEMENGYWCRKKQKQAGVNLTVGTPKDGSPDERWCFRVEEVNWSWQTLPT 720  
Db 661 KLQKAI SVLEMENGYWCRKKQKQAGVNLTVGTPKDGSPDERWCFRVEEVNWSWQTLPT 720  
QY 721 LCEDPSGAGVPRTELENPVLASPKDEDEGASEENYVPVQLQSN 764  
Db 721 LCEDPSGAGVPRTELENPVLASPKDEDEGASEENYVPVQLQSN 764

RESULT 9  
ID ABU04095  
XX AC ABU04095;  
XX DT 29-JAN-2003 (first entry)  
XX DE Human expressed protein tag (EPT) #761.  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX OS Homo sapiens.  
XX PN W0200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
XX PR 21-MAY-2001; 2001US-0292544P.  
XX PR 08-AUG-2001; 2001US-0310801P.  
XX PR 01-OCT-2001; 2001US-0326370P.  
XX PR 04-DEC-2001; 2001US-0336780P.  
XX PR 20-FEB-2002; 2002US-0358985P.  
XX PA (ZYCO-) ZYCOS INC.  
XX PI Chicx RM, Tomlinson AJ, Urban RG;  
XX DR WPI; 2003-040607/03.  
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukaemia.  
XX PS Example 2; SEQ ID NO 761; 134pp; English.  
XX CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 6; Length 764;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WTPSSSPVFRLETLDDGGQDSEADRGKLDGSGLPWMSQFQGEDRKFPQIRVNLNY 60  
Db 1 WTPSSSPVFRLETLDDGGQDSEADRGKLDGSGLPWMSQFQGEDRKFPQIRVNLNY 60  
QY 61 RKGTCASQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120  
Db 61 RKGTCASQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120  
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRGRHSALHIAIEKRSIQCVK 180  
Db 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRGRHSALHIAIEKRSIQCVK 180  
QY 181 LLVENGANVHARACGRFFQKGGCTCFYFGEPLSLAACTKQWDVVSYLLENPHQASLOA 240  
Db 181 LLVENGANVHARACGRFFQKGGCTCFYFGEPLSLAACTKQWDVVSYLLENPHQASLOA 240  
QY 241 TDSQNTVHLVHALVMSDNSAENIALVTSMDGLLQAGARLCTVQLEDIRNLQDITPLKL 300  
Db 241 TDSQNTVHLVHALVMSDNSAENIALVTSMDGLLQAGARLCTVQLEDIRNLQDITPLKL 300  
QY 301 AAKEGKIBIFRHILOREFSGLSHRKFTWCYGPVRSVLYDLASVDSCEENSVEIIFAF 360  
Db 301 AAKEGKIBIFRHILOREFSGLSHRKFTWCYGPVRSVLYDLASVDSCEENSVEIIFAF 360  
QY 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKPFNFCNLINFIETAVAYHQTPLKKQAA 420  
Db 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKPFNFCNLINFIETAVAYHQTPLKKQAA 420  
QY 421 PHLKAEVGNMLLTGHILILGGIYLLVGQWLYFWRHVFVWISFIDSYFELLFQALL 480  
Db 421 PHLKAEVGNMLLTGHILILGGIYLLVGQWLYFWRHVFVWISFIDSYFELLFQALL 480  
QY 481 TVVSQVLCFLAEWYLPPLVLSALVIGWLNLLYYTRGFQHTGIYSVMIOKVILRDLRLFL 540  
Db 481 TVVSQVLCFLAEWYLPPLVLSALVIGWLNLLYYTRGFQHTGIYSVMIOKVILRDLRLFL 540  
QY 541 IYLVFPGFAVALVSLQEARPEPTGNATESVQPMQDEGNGAQYRGILEASLEL 600  
Db 541 IYLVFPGFAVALVSLQEARPEPTGNATESVQPMQDEGNGAQYRGILEASLEL 600  
QY 601 FKFTIGMGLAFQELHFRGMVLLLLAYVLLTYILLNNMLIALMSETVNSVATDSWSIW 660  
Db 601 FKFTIGMGLAFQELHFRGMVLLLLAYVLLTYILLNNMLIALMSETVNSVATDSWSIW 660  
QY 661 KLQKAI SVLEMENGYWCRKKQKQAGVNLTVGTPKDGSPDERWCFRVEEVNWSWQTLPT 720  
Db 661 KLQKAI SVLEMENGYWCRKKQKQAGVNLTVGTPKDGSPDERWCFRVEEVNWSWQTLPT 720  
QY 721 LCEDPSGAGVPRTELENPVLASPKDEDEGASEENYVPVQLQSN 764  
Db 721 LCEDPSGAGVPRTELENPVLASPKDEDEGASEENYVPVQLQSN 764

RESULT 10  
ID ABU04104  
XX AC ABU04104 standard; protein; 764 AA.  
XX AC ABU04104;  
XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #770.  
 XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX OS Homo sapiens.  
 XX PN WO200278524-A2.  
 XX PD 10-OCT-2002.  
 XX PF 28-MAR-2002; 2002WO-US009671.  
 XX PR 28-MAR-2001; 2001US-0279495P.  
 XX PR 21-MAY-2001; 2001US-0292544P.  
 XX PR 08-AUG-2001; 2001US-0310801P.  
 XX PR 01-OCT-2001; 2001US-0326370P.  
 XX PR 04-DEC-2001; 2001US-0336780P.  
 XX PR 20-FEB-2002; 2002US-0358985P.  
 XX PA (ZYCO-) ZYCOS INC.  
 XX PI Chicz RM, Tomlinson AJ, Urban RG;  
 XX WPI; 2003-040607/03.  
 XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 XX PS Example 2; SEQ ID NO 770; 134pp; English.  
 XX CC The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 6; Length 764;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPSSSSPVFRLETLDDGGQDGESEADRGKLPFGSLPDMESQFQGEDRKFPQIRVNLNY 60  
 DB 1 MTPSSSSPVFRLETLDDGGQDGESEADRGKLPFGSLPDMESQFQGEDRKFPQIRVNLNY 60  
 QY 61 RKGTCASQPDNRRDRDLFNAVSRGVPEDLAAGLPEYLSKTSKYLTDSYEGSTGKTCL 120  
 DB 61 RKGTCASQPDNRRDRDLFNAVSRGVPEDLAAGLPEYLSKTSKYLTDSYEGSTGKTCL 120  
 QY 121 MKAVLNLDKGVNACILPLQLIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKSLQCVK 180  
 DB 121 MKAVLNLDKGVNACILPLQLIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKSLQCVK 180

QY 181 LLVENGANYHARACGRFFQKGGCTCFYFGELPLSLAACTKQWDVSVYLLENPHQPASLOA 240  
 DB 181 LLVENGANYHARACGRFFQKGGCTCFYFGELPLSLAACTKQWDVSVYLLENPHQPASLOA 240  
 QY 241 TDSQGNVTLHALVMSISDAENIALVTSYDGLLQAGARLCPVQLEDIRNLODLTPKL 300  
 DB 241 TDSQGNVTLHALVMSISDAENIALVTSYDGLLQAGARLCPVQLEDIRNLODLTPKL 300  
 QY 301 AAKGKIEIFRILQREFSGLSHRKFTWCYGPVRSYLYDIASVDSCEENSVLRIIAF 360  
 DB 301 AAKGKIEIFRILQREFSGLSHRKFTWCYGPVRSYLYDIASVDSCEENSVLRIIAF 360  
 QY 361 HCKSPHRHMVLEPLNKLLOAKWDLIIKPFNFNLCNLIYMFIFTAVAYHQTLKKQAA 420  
 DB 361 HCKSPHRHMVLEPLNKLLOAKWDLIIKPFNFNLCNLIYMFIFTAVAYHQTLKKQAA 420  
 QY 421 PHLKAEVGNMILLTGHIILGIIYLLVGOLMYFWRHVPIMISFIDSIFEILFLQALL 480  
 DB 421 PHLKAEVGNMILLTGHIILGIIYLLVGOLMYFWRHVPIMISFIDSIFEILFLQALL 480  
 QY 481 TVVSQVLCFLATEWYLPPLVLSALVGLWMLLYYTRGFQHTGIYSVMIQKVLRLDLRFL 540  
 DB 481 TVVSQVLCFLATEWYLPPLVLSALVGLWMLLYYTRGFQHTGIYSVMIQKVLRLDLRFL 540  
 QY 541 IYLVFLGFAVALVSLSQEAWRPEAPTGNATESVQPMEGQDEGNGAQYRGILEASLEL 600  
 DB 541 IYLVFLGFAVALVSLSQEAWRPEAPTGNATESVQPMEGQDEGNGAQYRGILEASLEL 600  
 QY 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
 DB 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
 QY 661 KLOKALSIVLEMENGYWCRKQKQAGVMTVGTGKDPGSDRWCFRVEEVNWSWEQTLPT 720  
 DB 661 KLOKALSIVLEMENGYWCRKQKQAGVMTVGTGKDPGSDRWCFRVEEVNWSWEQTLPT 720  
 QY 721 LCBDPSGAGVPRTPLENPVLASPPKDEDEGASEENYVPVQLQSN 764  
 DB 721 LCBDPSGAGVPRTPLENPVLASPPKDEDEGASEENYVPVQLQSN 764  
 RESULT 11  
 ABU04110  
 ID ABU04110 standard; protein; 764 AA.  
 AC ABU04110;  
 XX 29-JAN-2003 (first entry)  
 DT Human expressed protein tag (EPT) #776.  
 DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX OS Homo sapiens.  
 XX PN WO200278524-A2.  
 XX PD 10-OCT-2002.  
 XX PF 28-MAR-2002; 2002WO-US009671.  
 XX PR 28-MAR-2001; 2001US-0279495P.  
 XX PR 21-MAY-2001; 2001US-0292544P.  
 XX PR 08-AUG-2001; 2001US-0310801P.  
 XX PR 01-OCT-2001; 2001US-0326370P.  
 XX PR 04-DEC-2001; 2001US-0336780P.  
 XX PR 20-FEB-2002; 2002US-0358985P.  
 XX PA (ZYCO-) ZYCOS INC.

XX  
PI Chicz RM, Tomlinson AJ, Urban RG;  
XX  
XX WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 776; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 6; Length 764;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSFSSPVRLTLDGGQDSEADRGKLDGSLPPMESQFGEDRKFPAPQIRVNLNY 60  
DB 1 MTSFSSPVRLTLDGGQDSEADRGKLDGSLPPMESQFGEDRKFPAPQIRVNLNY 60

QY 61 RKGTGASQDPNPFDRDLFNASVSGVPEDLAGLPEVLSKTSKYLTDSEYTGSTGKTCL 120  
DB 61 RKGTGASQDPNPFDRDLFNASVSGVPEDLAGLPEVLSKTSKYLTDSEYTGSTGKTCL 120

QY 121 MKAVLNKGVNACILPLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSIQCVK 180  
DB 121 MKAVLNKGVNACILPLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSIQCVK 180

QY 181 LLVENGANVHARACGRPFQKGQCTCFYFGLPLSLAACTKQWDVSVLLENPHQPASLOA 240  
DB 181 LLVENGANVHARACGRPFQKGQCTCFYFGLPLSLAACTKQWDVSVLLENPHQPASLOA 240

QY 241 TDSQGNVTLHALVMSDNSAENIALVTSMDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300  
DB 241 TDSQGNVTLHALVMSDNSAENIALVTSMDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300

QY 301 AAKEGKIEIPRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360  
DB 301 AAKEGKIEIPRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360

QY 361 HCKSPHRRMVLEPLNKLQAKWDLIPKFFNELCNLYMFIETAVAVHQPATKQAA 420  
DB 361 HCKSPHRRMVLEPLNKLQAKWDLIPKFFNELCNLYMFIETAVAVHQPATKQAA 420

QY 421 PHLKAEGVNSMLTGHILLGGIYLLVQGLWTFWRHVFVWISFSDSYEILFLFQALL 480  
DB 421 PHLKAEGVNSMLTGHILLGGIYLLVQGLWTFWRHVFVWISFSDSYEILFLFQALL 480

QY 481 TVVSQVLCFLAIEWYLPPLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRDLRFL 540  
DB 481 TVVSQVLCFLAIEWYLPPLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRDLRFL 540

QY 541 IYLVFLFGFAVALVSLSQEAWRPEATGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600

DB 541 IYLVFLFGFAVALVSLSQEAWRPEATGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600

QY 601 FKFTTGMGELAFQEQHFRGMVLLLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660  
DB 601 FKFTTGMGELAFQEQHFRGMVLLLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660

QY 661 KLOKAISVLEWNGYWCCKKQKORAGVMLTVGTPKDGSPDERWCERVEVNWASWEQTLP 720  
DB 661 KLOKAISVLEWNGYWCCKKQKORAGVMLTVGTPKDGSPDERWCERVEVNWASWEQTLP 720

QY 721 LCEDPSGAGVPTLENPNVLASPPKEDDEGCASENYPVQLQSN 764  
DB 721 LCEDPSGAGVPTLENPNVLASPPKEDDEGCASENYPVQLQSN 764

RESULT 12  
ABU04106  
ID ABU04106 standard; protein; 764 AA.  
XX  
AC ABU04106;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #772.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
PA (ZYCO-) ZYCOS INC.  
XX  
PI Chicz RM, Tomlinson AJ, Urban RG;  
XX  
XX WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 772; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 6; Length 764;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSFSSPVFRLETLGGQDGEADRGKLDGSGLPMPMESQFGEDRKFPAPQIRVNLNY 60  
DB 1 MTSFSSPVFRLETLGGQDGEADRGKLDGSGLPMPMESQFGEDRKFPAPQIRVNLNY 60  
QY 61 RKTGASQDPNFRDRDLFNNAVSRGVPEDLAGLPEYLSKTYLTDSEYESTGKTCL 120  
DB 61 RKTGASQDPNFRDRDLFNNAVSRGVPEDLAGLPEYLSKTYLTDSEYESTGKTCL 120  
QY 121 MKAVLNKDGVNACILPLLQIDRDGSGNPQPLVNAQCTDDYYRGSALHIAIEKRSQCCK 180  
DB 121 MKAVLNKDGVNACILPLLQIDRDGSGNPQPLVNAQCTDDYYRGSALHIAIEKRSQCCK 180  
QY 181 LLVENGANVHARACGRFFQKGQTCFYFGBELPLSLAACTKQWDVSVYLLNPHQPASLQA 240  
DB 181 LLVENGANVHARACGRFFQKGQTCFYFGBELPLSLAACTKQWDVSVYLLNPHQPASLQA 240  
QY 241 TDSQNTVLHALVMSNSAENIALVTSMYDGLQAGARLCPVQLEDIRNLDLPLKL 300  
DB 241 TDSQNTVLHALVMSNSAENIALVTSMYDGLQAGARLCPVQLEDIRNLDLPLKL 300  
QY 301 AAKGKTEIPRHILQREFSGLSHLSKFTWCYGVRSVLYDLASVDSCENSVELEIAF 360  
DB 301 AAKGKTEIPRHILQREFSGLSHLSKFTWCYGVRSVLYDLASVDSCENSVELEIAF 360  
QY 361 HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAVAYHPTLKKQAA 420  
DB 361 HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAVAYHPTLKKQAA 420  
QY 421 PHLKAEGVNSMLTGHILILGGIYLLVQGLWYFRRHVFIIWISFIDSYFEILFQALL 480  
DB 421 PHLKAEGVNSMLTGHILILGGIYLLVQGLWYFRRHVFIIWISFIDSYFEILFQALL 480  
QY 481 TVVSQVLCFLAIEWYLLPVSALVGLWNLIIYTRGFQHTGIYSVMIQKVLIRDLRLFL 540  
DB 481 TVVSQVLCFLAIEWYLLPVSALVGLWNLIIYTRGFQHTGIYSVMIQKVLIRDLRLFL 540  
QY 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQGEDEGNGAQYRGILEASLEL 600  
DB 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQGEDEGNGAQYRGILEASLEL 600  
QY 601 FKFTIGMGEIAFQBLHFRGMVLLLLAYVLLTYILLNMLIALMSTVNSVATDSWSIW 660  
DB 601 FKFTIGMGEIAFQBLHFRGMVLLLLAYVLLTYILLNMLIALMSTVNSVATDSWSIW 660  
QY 661 KLOKAIISVLENGYVWCRKQKQAGVMTVCTKPDGSDRWCPRVEEVNWSWEQTLPT 720  
DB 661 KLOKAIISVLENGYVWCRKQKQAGVMTVCTKPDGSDRWCPRVEEVNWSWEQTLPT 720  
QY 721 LCEDPGAGVPRILENVLASPPKDEDEGASEENYVPVQLLQSN 764  
DB 721 LCEDPGAGVPRILENVLASPPKDEDEGASEENYVPVQLLQSN 764

RESULT 13  
ABU04096  
ID ABU04096 standard; protein; 764 AA.  
XX  
AC ABU04096;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #762.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
XX (ZYCO-) ZYCOS INC.  
XX  
XX Chiciz RM, Tomlinson AJ, Urban RG;  
XX  
XX WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 762; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 6; Length 764;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSFSSPVFRLETLGGQDGEADRGKLDGSGLPMPMESQFGEDRKFPAPQIRVNLNY 60  
DB 1 MTSFSSPVFRLETLGGQDGEADRGKLDGSGLPMPMESQFGEDRKFPAPQIRVNLNY 60  
QY 61 RKTGASQDPNFRDRDLFNNAVSRGVPEDLAGLPEYLSKTYLTDSEYESTGKTCL 120  
DB 61 RKTGASQDPNFRDRDLFNNAVSRGVPEDLAGLPEYLSKTYLTDSEYESTGKTCL 120  
QY 121 MKAVLNKDGVNACILPLLQIDRDGSGNPQPLVNAQCTDDYYRGSALHIAIEKRSQCCK 180  
DB 121 MKAVLNKDGVNACILPLLQIDRDGSGNPQPLVNAQCTDDYYRGSALHIAIEKRSQCCK 180  
QY 181 LLVENGANVHARACGRFFQKGQTCFYFGBELPLSLAACTKQWDVSVYLLNPHQPASLQA 240  
DB 181 LLVENGANVHARACGRFFQKGQTCFYFGBELPLSLAACTKQWDVSVYLLNPHQPASLQA 240

Db 181 LLVENGANVHARACGRFFQKQGTCTFYFGEPLSLAACTKQWDVSVYLLLENPHQPASLOA 240  
 Qy 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLAGARLCPTVQLEDIRNLQDLTPLKL 300  
 Db 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLAGARLCPTVQLEDIRNLQDLTPLKL 300  
 Qy 301 AAKEGKIEIFRHLQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLIIAF 360  
 Db 301 AAKEGKIEIFRHLQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLIIAF 360  
 Qy 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKFFNLCNLIIYMFIFTAAYHPTLKKQAA 420  
 Db 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKFFNLCNLIIYMFIFTAAYHPTLKKQAA 420  
 Qy 421 PHLKAEVGNMMLTGHLILGGIYLLVQGLWYFMRHVPFIWTSFIDSYPFELFLFOALL 480  
 Db 421 PHLKAEVGNMMLTGHLILGGIYLLVQGLWYFMRHVPFIWTSFIDSYPFELFLFOALL 480  
 Qy 481 TVVSQVLCFLAIEWYLLPLVLSALVGLWNLIIYTRGFQHTGIYSVMIOKVILDLIRFL 540  
 Db 481 TVVSQVLCFLAIEWYLLPLVLSALVGLWNLIIYTRGFQHTGIYSVMIOKVILDLIRFL 540  
 Qy 541 IYLVFLFGFAVALVLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQRGILEASLEL 600  
 Db 541 IYLVFLFGFAVALVLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQRGILEASLEL 600  
 Qy 601 FKFTIGMGLAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
 Db 601 FKFTIGMGLAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660  
 Qy 661 KLOKATSVLEMENGYWCRKQKQAGVMTVGTKPDGSPDERWCFRVEEWNASWEQTLPT 720  
 Db 661 KLOKATSVLEMENGYWCRKQKQAGVMTVGTKPDGSPDERWCFRVEEWNASWEQTLPT 720  
 Qy 721 LCDPDSGAGVPRTELENPLVLPASPKPEDEGNGAENYVPVQLQSN 764  
 Db 721 LCDPDSGAGVPRTELENPLVLPASPKPEDEGNGAENYVPVQLQSN 764

RESULT 14

AD181598  
 ID AD181598 standard; protein; 764 AA.

XX AC AD181598;

XX DT 22-APR-2004 (first entry)

XX DE Human vanilloid receptor-like protein 1 #2.

XX KW Human; calcium entry modulator; CD4536; CD5842; intracellular calcium; neurological disease; inflammatory disease; cancer; Alzheimer's disease; Parkinson's disease; asthma; rheumatoid arthritis; liver disease; hepatitis; cirrhosis; kidney disease; glomerulonephritis.

OS Homo sapiens.

XX US2004009537-A1.

XX 15-JAN-2004.

XX 13-JAN-2003; 2003US-00342844.

XX 11-JAN-2002; 2002US-0347459P.

XX 02-AUG-2002; 2002US-0401171P.

XX 20-AUG-2002; 2002US-0405678P.

XX (ROOS/) ROOS J.

XX (STAU/) STAUDERMAN K.

XX (VELI/) VELICELEBI G.

XX Roos J, Stauderman K, Velicelebi G;

XX WPI; 2004-090465/09.

DR N-PSDB; AD181597.  
 XX Identifying an agent that modulates intracellular calcium levels, useful for treating diseases associated with calcium dysregulation (e.g. cancer), comprises monitoring the effects of the agent on store-operated calcium entry.

PS Disclosure; SEQ ID NO 68; 55pp; English.

XX The invention relates to identifying an agent that modulates intracellular calcium comprises monitoring the effects of the agent on store-operated calcium entry comprising contacting one or more test cells or their portion comprising one or more proteins that is (are) at least about 35% homologous to the protein encoded by Drosophila gene CG4536 or CG5842 over at least about 40% of the encoded protein (and that provides for store-operated calcium entry with a test agent), where the portion of the cell comprises the proteins, monitoring the effect(s) of the test compound on store-operated calcium entry and identifying a test agent as an agent if it has an effect on store-operated calcium entry. Also included are a method of modulating store-operated calcium entry (comprising modulating the level of, expression of, activity of or molecular interactions of a protein in a cell that has altered store-operated calcium entry, where the protein is at least about 35% homologous to the protein encoded by Drosophila gene CG4536 or CG5842 over at least about 40% of the encoded protein and that provides for store-operated calcium entry, and where store-operated calcium transport into the cell is modulated) and a method of identifying a molecule that provides for store-operated calcium entry (comprising identifying a molecule that interacts with the protein mentioned above, thus, identifying molecules involved in modulating store-operated calcium entry. The protein does not contain the contiguous sequences appearing as AD181644 and AD181645. The proteins are selected from ion transport proteins. The method is useful in modulating, or in identifying agents that modulate, intracellular calcium. These may be used in treating diseases associated with calcium dysregulation, such as neurodegenerative diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases (e.g. hepatitis or cirrhosis) or kidney diseases (e.g. glomerulonephritis). The present sequence represents an identified homologue of one of the two above mentioned drosophila proteins.

XX SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 8; Length 764;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTPSSSPVFRLETLDGGQDSEADRGKLDGSGLPMPESQFQGEDRKFAPIRVNLNY 60  
 Db 1 MTPSSSPVFRLETLDGGQDSEADRGKLDGSGLPMPESQFQGEDRKFAPIRVNLNY 60  
 Qy 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 120  
 Db 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 120  
 Qy 121 MKAVLNKDGVNACILPILQIDRDSGNPQPLVNAQCTDDYRGHSALHIAIKRSIQCVK 180  
 Db 121 MKAVLNKDGVNACILPILQIDRDSGNPQPLVNAQCTDDYRGHSALHIAIKRSIQCVK 180  
 Qy 181 LLVENGANVHARACGRFFQKQGTCTFYFGEPLSLAACTKQWDVSVYLLLENPHQPASLOA 240  
 Db 181 LLVENGANVHARACGRFFQKQGTCTFYFGEPLSLAACTKQWDVSVYLLLENPHQPASLOA 240  
 Qy 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLAGARLCPTVQLEDIRNLQDLTPLKL 300  
 Db 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLAGARLCPTVQLEDIRNLQDLTPLKL 300  
 Qy 301 AAKEGKIEIFRHLQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLIIAF 360  
 Db 301 AAKEGKIEIFRHLQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLIIAF 360  
 Qy 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKFFNLCNLIIYMFIFTAAYHPTLKKQAA 420



361 HCKSPHRRMVVLEPLNKLQAKWDLIPKFFLNLNLYMFIPTAVAYHPTLKQAA 420  
421 PHLKAEGVNSMLLTGHILILGGIYLLVQWLYFWRHVFVWISFIDSYPEILFLFOALL 480  
421 PHLKAEGVNSMLLTGHILILGGIYLLVQWLYFWRHVFVWISFIDSYPEILFLFOALL 480  
481 TVVSQVLCFLAIEWYLLVLSALVGLWNLVLYYTRGFQHTGIYSVMQVILRDLRLFL 540  
481 TVVSQVLCFLAIEWYLLVLSALVGLWNLVLYYTRGFQHTGIYSVMQVILRDLRLFL 540  
541 IYLVFLGFAVALVLSQEAWRPEAPTGNATESVOPMEQDEGNGAQRGILEASLEL 600  
541 IYLVFLGFAVALVLSQEAWRPEAPTGNATESVOPMEQDEGNGAQRGILEASLEL 600  
601 FKFTIGWGLAFOELHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660  
601 FKFTIGWGLAFOELHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660  
661 KLOKALSVLEMENGYWCRKQKQAGVMLTVGTPDGSPPDERWCFRVEEVNWSWEQTLPT 720  
661 KLOKALSVLEMENGYWCRKQKQAGVMLTVGTPDGSPPDERWCFRVEEVNWSWEQTLPT 720  
721 LCEDPGAGVPRTLENPVLASPPKEDDGEASEENYVPVQLQSN 764  
721 LCEDPGAGVPRTLENPVLASPPKEDDGEASEENYVPVQLQSN 764

RESULT 15

ID ADP66663  
XX ADP66663 standard; protein; 764 AA.  
AC ADP66663;  
XX  
XX 26-AUG-2004 (first entry)  
XX Human vanilloid 2 receptor (VR2) polypeptide, SEQ ID 2.  
XX  
XX VR2; vanilloid 2 receptor; tranquilizer; antidepressant; hypnotic; CNS;  
KW tocolytic; vasotropic; hypotensive; cardiovascular; gynaecological;  
KW analgesic; neuroleptic; anticoagulant; gene therapy; human; receptor.  
XX  
XX Homo sapiens.  
XX  
XX W02004045638-A1.  
XX  
XX 03-JUN-2004.  
XX  
XX 18-NOV-2003; 2003WO-GB004988.  
XX  
XX 18-NOV-2002; 2002GB-00026850.  
XX  
XX 18-NOV-2002; 2002GB-00026865.  
XX  
XX 01-OCT-2003; 2003GB-00022990.  
XX  
XX (MERI ) MERCK SHARP & DOHME LTD.  
XX  
XX Oliver KR, Seabrook GR, Wainwright A;  
XX  
XX WPI; 2004-431843/40.  
XX  
XX N-PSDB; ADP66662.

Use of vanilloid receptor-2 ligands for treating and/or preventing anxiety, depression, circadian rhythm disorders, pre-term labor, erectile dysfunction, hypertension, eclampsia and/or schizophrenia.  
Claim 20; Fig 1; 46pp; English.  
The invention relates to a compound selected from a vanilloid 2 receptor (VR2) polypeptide, a compound which modulates the activity of a VR2 polypeptide, a polynucleotide encoding a VR2 polypeptide, or an antisense polynucleotide. The compound is used for the manufacture of a medicament for treating anxiety, depression, circadian rhythm disorders, pre-term labour, erectile dysfunction, hypertension and/or eclampsia and associated disorders, and/or schizophrenia. The compound may also be used

for inducing diuresis and/or inhibiting platelet agglutination. The compound may also be used for manufacturing a medicament for treating the disorders mentioned above. The medicament enhances or improves sleep quality and/or is used for preventing and/or treating sleep disorders and sleep disturbances by increasing sleep efficiency and augmenting sleep maintenance in a mammal, or for achieving a circadian rhythm phase-shifting effect, for resetting the internal circadian clock or for shortening the time of reentrainment of circadian rhythms in a mammal. The present sequence represents a human VR2 polypeptide.

SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 8; Length 764;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPSSSPVFRLETLDDGGEDGSEADRGKLDGSGLPMMESQFQGEDRKFAPQIRVNLNY 60  
DB 1 MTPSSSPVFRLETLDDGGEDGSEADRGKLDGSGLPMMESQFQGEDRKFAPQIRVNLNY 60  
QY 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120  
DB 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120  
QY 121 MKAVNLKDGVNACILPLQLIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSQCVR 180  
DB 121 MKAVNLKDGVNACILPLQLIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSQCVR 180  
QY 181 LLVENGANVHARACGRFFQGGTCTFYFGEPLSLAACTKQWDVSVLLENPHQASLOA 240  
DB 181 LLVENGANVHARACGRFFQGGTCTFYFGEPLSLAACTKQWDVSVLLENPHQASLOA 240  
QY 241 TDSQGNVTLHALVMSIDNSAENIALVTSYDGLQAGARLCPTVQLIEDIRNLQDLTPLKL 300  
DB 241 TDSQGNVTLHALVMSIDNSAENIALVTSYDGLQAGARLCPTVQLIEDIRNLQDLTPLKL 300  
QY 301 AAKEGKIEIFRHLQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF 360  
DB 301 AAKEGKIEIFRHLQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF 360  
QY 361 HCKSPHRRMVVLEPLNKLQAKWDLIPKFFLNLNLYMFIPTAVAYHPTLKQAA 420  
DB 361 HCKSPHRRMVVLEPLNKLQAKWDLIPKFFLNLNLYMFIPTAVAYHPTLKQAA 420  
QY 421 PHLKAEGVNSMLLTGHILILGGIYLLVQWLYFWRHVFVWISFIDSYPEILFLFOALL 480  
DB 421 PHLKAEGVNSMLLTGHILILGGIYLLVQWLYFWRHVFVWISFIDSYPEILFLFOALL 480  
QY 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLVLYYTRGFQHTGIYSVMQVILRDLRLFL 540  
DB 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLVLYYTRGFQHTGIYSVMQVILRDLRLFL 540  
QY 541 IYLVFLGFAVALVLSQEAWRPEAPTGNATESVOPMEQDEGNGAQRGILEASLEL 600  
DB 541 IYLVFLGFAVALVLSQEAWRPEAPTGNATESVOPMEQDEGNGAQRGILEASLEL 600  
QY 601 FKFTIGWGLAFOELHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660  
DB 601 FKFTIGWGLAFOELHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660  
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DB 661 KLOKALSVLEMENGYWCRKQKQAGVMLTVGTPDGSPPDERWCFRVEEVNWSWEQTLPT 720  
QY 721 LCEDPGAGVPRTLENPVLASPPKEDDGEASEENYVPVQLQSN 764  
DB 721 LCEDPGAGVPRTLENPVLASPPKEDDGEASEENYVPVQLQSN 764

Search completed: October 5, 2005, 11:23:48  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 17:21:10 ; Search time 431 Seconds  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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		Match	Length	DB		
1	2424.6	98.2	2805	3	US-09-132-316-1	Sequence 1, Appli
2	2378.4	96.3	2380	3	US-09-235-451-35	Sequence 35, Appl
3	2378.4	96.3	2380	4	US-09-978-303-35	Sequence 35, Appl
4	2259.2	91.5	2779	3	US-09-149-476-191	Sequence 191, App
5	2061.8	83.5	2860	3	US-09-149-476-314	Sequence 314, App
6	1720	69.7	1790	3	US-09-484-970B-67	Sequence 67, Appli
7	1522.4	61.7	2736	3	US-09-235-451-3	Sequence 3, Appli
8	1522.4	61.7	2736	4	US-09-978-303-3	Sequence 3, Appli
9	750.8	30.4	884	3	US-09-235-451-22	Sequence 22, Appl
10	750.8	30.4	884	4	US-09-978-303-22	Sequence 22, Appl
11	711	28.8	876	3	US-09-149-476-315	Sequence 315, App
12	662.4	26.8	4182	4	US-09-667-422-2	Sequence 2, Appli
13	662.4	26.8	4203	4	US-09-667-422-1	Sequence 1, Appli
14	660.8	26.8	2544	3	US-09-235-451-33	Sequence 33, Appl
15	660.8	26.8	2544	4	US-09-978-303-33	Sequence 33, Appl
16	660.8	26.8	3500	3	US-09-197-636-7	Sequence 7, Appli
17	660.8	26.8	4803	3	US-09-197-636-1	Sequence 1, Appli
18	660	26.7	4803	3	US-09-197-636-3	Sequence 3, Appli
19	659.2	26.7	3263	3	US-09-949-016-1066	Sequence 1066, Ap
20	659.2	26.7	3463	3	US-09-533-220A-1	Sequence 1, Appli
21	651.8	26.4	2633	3	US-09-667-422-8	Sequence 8, Appli
22	651.8	26.4	2880	3	US-09-235-451-1	Sequence 1, Appli
23	651.8	26.4	2880	4	US-09-978-303-1	Sequence 1, Appli
24	650	26.3	4171	4	US-09-667-422-3	Sequence 3, Appli
25	597.6	24.2	764	3	US-09-235-451-21	Sequence 21, Appl
26	597.6	24.2	764	3	US-09-978-303-21	Sequence 21, Appl
27	578	21.4	768	3	US-09-235-451-6	Sequence 6, Appli

## ALIGNMENTS

## RESULT 1

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US-09-132-316-1
; Sequence 1, Application US/09132316B
;
; Patent No. 6444440
; GENERAL INFORMATION:
;
; APPLICANT: Young, Paul E.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Vanilloid Receptor-2
; FILE REFERENCE: 1488.111000
; CURRENT APPLICATION NUMBER: US/09/132,316B
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: US 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5)..(2674)
; US-09-132-316-1

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Best Local Similarity 99.4%; Pred. No. 0;  
Matches 2455: Conservative 0; Mismatches 9; Indels 5; Gaps 2

Qy	3	CGAGGCCGACGCGACGTGGGAGGAGACAGGACCCCTTGACATCTCATCTGTCACAGG	62
Db	287	CAACACCGACGCCACGTGGGAGGAGACAGGACCCCTTGACATCTCATCTGTCACAGG	346
Qy	63	TCCTGCTGTCGACCGAGC--AGCCTCCTCTCTAGATGACCTCACCCCTCCAGCTCTCCA	120
Db	347	TCCTGCTGACCGAGCTATGCCTCTCTCTAGATGACCTCACCCCTCCAGCTCTCCA	406
Qy	121	GTTTTCAGGTTGAGACATTTAGATGGAGGCCAAGAGATGGCTCTGAGGCCGACAGGGA	180
Db	407	GTTTTCAGGTTGAGACATTTAGATGGAGGCCAAGAGATGGCTCTGAGGCCGACAGGGA	466
Qy	181	AAGCTGGATTTTCGGAGCGGGCTGCCTCCATGGAGTCACAGTTCCAGGGCGGAGACCGG	240
Db	467	AAGCTGGATTTTCGGAGCGGGCTGCCTCCATGGAGTCACAGTTCCAGGGCGGAGACCGG	526
Qy	241	AAATTCGCCCTCCAGATAAGAGTCAACCTCAACTTACCGAAAGGGAACAGGTGCCAGTCAG	300
Db	527	AAATTCGCCCTCCAGATAAGAGTCAACCTCAACTTACCGAAAGGGAACAGGTGCCAGTCAG	586



Db	2744	GGTCCAGT	2752	Db	541	AGTCTGCAGTGTGTGAAGCTCCTGGTGGAGATGGGGCCAAATGTGTGCATCCCGGGGCTTC	600
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US-09-235-451-35							
; Sequence 35, Application US/09235451							
; GENERAL INFORMATION:							
; APPLICANT: Julius, David J.							
; APPLICANT: Caterina, Michael J.							
; APPLICANT: Brake, Anthony J.							
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING							
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED							
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF							
; FILE REFERENCE: 9076/084CIP							
; CURRENT APPLICATION NUMBER: US/09/235,451							
; CURRENT FILING DATE: 1999-01-22							
; PRIOR APPLICATION NUMBER: 60/072,151							
; PRIOR FILING DATE: 1998-01-22							
; PRIOR APPLICATION NUMBER: 08/915,461							
; PRIOR FILING DATE: 1997-08-20							
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; SEQ ID NO 35							
; LENGTH: 2380							
; TYPE: DNA							
; ORGANISM: Homo sapiens							
; FEATURE:							
; NAME/KEY: CDS							
; LOCATION: (19)...(2313)							
; OTHER INFORMATION: Human VR2							
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Best Local Similarity				100.0%; Pred. No. 0;			
Matches 2379; Conservative				0; Mismatches 1; Indels 0; Gaps 0;			
QY	79	CAGCCTCTCTCTCTAGGATGACTCACCTCCAGCTCTCAGTCTTCAGTCTTCAGGTTGGAGACA	138	QY	541	AGTCTGCAGTGTGTGAAGCTCCTGGTGGAGATGGGGCCAAATGTGTGCATCCCGGGGCTTC	600
Db	1	CAGCTCTCTCTCTCTAGGATGACTCACCTCCAGCTCTCAGTCTTCAGTCTTCAGGTTGGAGACA	60	QY	679	GGCCGCTTCTTCCAGAAGGGCCAAAGGACTTCTCTTTATTTTCGGTGAGCTACCCCTCTCT	738
QY	139	TTAGATGGAGGCCAAGAAGATGCTCTGAGCGCGACAGAGAAAGCTGGATTTGGAGC	198	Db	601	GGCCGCTTCTTCCAGAAGGGCCAAAGGACTTCTCTTTATTTTCGGTGAGCTACCCCTCTCT	660
Db	61	TTAGATGGAGGCCAAGAAGATGCTCTGAGCGCGACAGAGAAAGCTGGATTTGGAGC	120	QY	739	TTGGCCGCTTGCACCAAGCAGTGGATGTGTAAGCTACCTCTCGAGAACCCACACACAG	798
QY	199	GGCGTCTCCATGAGTACAGTTCAGGCGAGGACCGGAATTCGCCCTCAGATA	258	Db	661	TTGGCCGCTTGCACCAAGCAGTGGATGTGTAAGCTACCTCTCGAGAACCCACACACAG	720
Db	121	GGCGTCTCTCCATGAGTACAGTTCAGGCGAGGACCGGAATTCGCCCTCAGATA	180	QY	799	CCCGCAGCTGCAGGCCACTGACTCCAGGGGCAACAGTCTCTGATCCCTAGTAGTG	858
QY	259	AGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCCAGTCAGCGGATCCAAACCGATTT	318	Db	721	CCCGCAGCTGCAGGCCACTGACTCCAGGGGCAACAGTCTCTGATCCCTAGTAGTG	780
Db	181	AGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCCAGTCAGCGGATCCAAACCGATTT	240	QY	859	ATCTCGGACAACTCAGCTGAGAACATTGCACTGGTGACCAAGATGTATGATGGGCTCCTC	918
QY	319	GACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTCTCCCGAGGATCTGGTGACTT	378	Db	781	ATCTCGGACAACTCAGCTGAGAACATTGCACTGGTGACCAAGATGTATGATGGGCTCCTC	840
Db	241	GACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTCTCCCGAGGATCTGGTGACTT	300	QY	919	CAAGCTGGGGCCCGCTCTGCCCCCTACCGTGCACTTGGAGCAATCCGCAACCTGCAAGGAT	978
QY	379	CCAGGTACCTGAGCAAGACAGCAAGTACTCACCGACTCGGAATACAGAGGGCTCC	438	Db	841	CAAGCTGGGGCCCGCTCTGCCCCCTACCGTGCACTTGGAGCAATCCGCAACCTGCAAGGAT	900
Db	301	CCAGGTACCTGAGCAAGACAGCAAGTACTCACCGACTCGGAATACAGAGGGCTCC	360	QY	979	CTCAGCCTCTGAAGCTGCGCCCGCAAGGAGGGCAAGATCGAGATTTTCAGGCAATCTCTG	1038
QY	439	ACAGGTAAAGCTGCGCTGATGAAGCTGTGCTGAACCTTAAGGACGGAGTCAATGCTCTGC	498	Db	901	CTCAGCCTCTGAAGCTGCGCCCGCAAGGAGGGCAAGATCGAGATTTTCAGGCAATCTCTG	960
Db	361	ACAGGTAAAGCTGCGCTGATGAAGCTGTGCTGAACCTTAAGGACGGAGTCAATGCTCTGC	420	QY	1039	CAGCGGAGTTTTCAGGACTGAGCCACTTTCCGAAAGTTCCACCGAGTGTCTATGGG	1098
QY	499	ATTCTGCGCACTGTCTGAGATCGACAGGGACTCTGGCAATCTCAGCCCTTGGTAATGCC	558	Db	961	CAGCGGAGTTTTCAGGACTGAGCCACTTTCCGAAAGTTCCACCGAGTGTCTATGGG	1020
Db	421	ATTCTGCGCACTGTCTGAGATCGACAGGGACTCTGGCAATCTCAGCCCTTGGTAATGCC	480	QY	1099	CTGTCCGGGTGTGCTGTATGACCTTGACCTTCTGTGGACAGCTGTGAGGAGAACTCAGTG	1158
QY	559	CAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCACATCGGCCATTGAGAAGG	618	Db	1021	CTGTCCGGGTGTGCTGTATGACCTTCTGTGGACAGCTGTGAGGAGAACTCAGTG	1080
Db	481	CAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCACATCGGCCATTGAGAAGG	540	QY	1159	CTGGAGATCATTTGCCCTTTCAITTCAGAGAGCCCGCACCGAATGGTCTGTTTGGAG	1218
QY	619	AGTCTGCAGTGTGTGAAGCTCTCTGGTGGAGAAATGGGGCCAAATGTGCATGCCCGGCTGC	678	Db	1081	CTGGAGATCATTTGCCCTTTCAITTCAGAGAGCCCGCACCGAATGGTCTGTTTGGAG	1140



Qy	1039	CAGCGGAGT	TTTTCAGGACTGAGCCACCTTTCCGAAAGTTTACCGAGTGGTGCTATGGG	1099
Db	961	CAGCGGAGT	TTTTCAGGACTGAGCCACCTTTCCGAAAGTTTACCGAGTGGTGCTATGGG	1020
Qy	1099	CTGTCCGGGTGTCGTGTATGACCTGGCTTCTGTGGACAGCTGTGAGGAGAACTCAGTGG	1158	
Db	1021	CTGTCCGGGTGTCGTGTATGACCTGGCTTCTGTGGACAGCTGTGAGGAGAACTCAGTGG	1080	
Qy	1159	CTGAGAGATCAATGGCTTTTCAATTGCAAGAGCCGACCGACACCGAATGGTTCGTTTGGGAG	1218	
Db	1081	CTGAGAGATCAATGGCTTTTCAATTGCAAGAGCCGACCGACACCGAATGGTTCGTTTGGGAG	1140	
Qy	1219	CCCCTGAACAAACTGTCTGCAAGGGGAAATGGGATCTGTCTCATCCCAAGTTCCTTTAAAC	1278	
Db	1141	CCCCTGAACAAACTGTCTGCAAGGGGAAATGGGATCTGTCTCATCCCAAGTTCCTTTAAAC	1200	
Qy	1279	TTCTCTGTGAATCTGAATCAATGTTTCATCTTCCACCGCTGTGCCTACCATCAGCCTTACC	1338	
Db	1301	TTCTCTGTGAATCTGAATCAATGTTTCATCTTCCACCGCTGTGCCTACCATCAGCCTTACC	1260	
Qy	1339	CTGAAGAAGCAGGCGCGCCCTCACCTGAAAGCGAGGTTGGAAATCTCATGTCTGTGACG	1398	
Db	1261	CTGAAGAAGCAGGCGCGCCCTCACCTGAAAGCGAGGTTGGAAATCTCATGTCTGTGACG	1320	
Qy	1399	GGCCACATCTCTTATCTCTGCTAGGGGGGANTCTACTCTCTGTGGGCCAGCTGTGGTACTTTC	1458	
Db	1321	GGCCACATCTCTTATCTCTGCTAGGGGGGANTCTACTCTCTGTGGGCCAGCTGTGGTACTTTC	1380	
Qy	1459	TGGCGGCGCCACAGTGTTCATCTGATCTCGTTTCATAGACAGCTACTTTGAAATCTCTCTTC	1518	
Db	1381	TGGCGGCGCCACAGTGTTCATCTGATCTCGTTTCATAGACAGCTACTTTGAAATCTCTCTTC	1440	
Qy	1519	CTGTTTCAGGCCCCTGTCTCACAGTGGTGTCCAGGTGCTGTGTTTCTTGGCCATCGAGTGG	1578	
Db	1441	CTGTTTCAGGCCCCTGTCTCACAGTGGTGTCCAGGTGCTGTGTTTCTTGGCCATCGAGTGG	1500	
Qy	1579	TACCTGGCCCTGTGTGTCTGCCCTGGTGTCTGGGCTGGCTGAACCTGCTTTACTATACA	1638	
Db	1501	TACCTGGCCCTGTGTGTCTGCCCTGGTGTCTGGGCTGGCTGAACCTGCTTTACTATACA	1560	
Qy	1639	CGTGGCTTCCAGCACACAGGCATCTACAGTGTCTATGATCCAGAAGGTCTATCTTCGGGGAC	1698	
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Qy	1699	CTGCTGGCCTTCTTCTGATCTATCTAGTCTTCTCTTTTCGGCTTCGCTGTAGCCCTGGTG	1758	
Db	1621	CTGCTGGCCTTCTTCTGATCTATCTAGTCTTCTCTTTTCGGCTTCGCTGTAGCCCTGGTG	1680	
Qy	1759	AGCCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCCTACAGSCCCCAATGCCACAGAGTCA	1818	
Db	1681	AGCCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCCTACAGSCCCCAATGCCACAGAGTCA	1740	
Qy	1819	GTGCAGCCCATGAGGGGACAGGAGGACGAGGGCCACCGGGGCCAGTACAGGGGTATCCTTG	1878	
Db	1741	GTGCAGCCCATGAGGGGACAGGAGGACGAGGGCCACCGGGGCCAGTACAGGGGTATCCTTG	1800	
Qy	1879	GAAGCCTCTTTGGAGCTCTTCAAAATCACCATCGGCATGGCGAGCTGGCCCTCCAGGAG	1938	
Db	1801	GAAGCCTCTTTGGAGCTCTTCAAAATCACCATCGGCATGGCGAGCTGGCCCTCCAGGAG	1860	
Qy	1939	CAGCTGCATCTTCCGGGCAATGGTGTCTGTCTGTCTGGGCTTACGTGCTCACTCACCTAC	1998	
Db	1861	CAGCTGCATCTTCCGGGCAATGGTGTCTGTCTGTCTGGGCTTACGTGCTCACTCACCTAC	1920	
Qy	1999	ATCTCTGTCTCAACATGCTCATCGCCCTCATAGAGCGAGACCGTCAACAGTGTGCCACT	2058	
Db	1921	ATCTCTGTCTCAACATGCTCATCGCCCTCATAGAGCGAGACCGTCAACAGTGTGCCACT	1980	
Qy	2059	GACAGCTGGAGCATCTGGAGCTGCAGAAAGCCATCTCTGTCTGGAGTGGGAATGGC	2118	
Db	1981	GACAGCTGGAGCATCTGGAGCTGCAGAAAGCCATCTCTGTCTGGAGTGGGAATGGC	2040	

Qy	2119	TATTGGTGTGTCAGGAAGACAGCGGCAGGTGTGATGCTGACCGTTGGCACTAAGCCA	2179
Db	2041	TATTGGTGTGTCAGGAAGACAGCGGCAGGTGTGATGCTGACCGTTGGCACTAAGCCA	2100
Qy	2179	GATGGCAGCCCGATGATGACGCTGTGTCTTCAGGGTGGAGGAGGTGAACCTGGGCTTCATGG	2238
Db	2101	GATGGCAGCCCGATGATGACGCTGTGTCTTCAGGGTGGAGGAGGTGAACCTGGGCTTCATGG	2160
Qy	2239	GACGACAGCTGCCTACGCTGTGTGAGGACCCCGTCAGGGCAGGTGTCTCGAACTCTC	2298
Db	2161	GACGACAGCTGCCTACGCTGTGTGAGGACCCCGTCAGGGCAGGTGTCTCGAACTCTC	2220
Qy	2299	GAGAACCTGTCTGGCTTCCCTCCCAAGGAGGATGAGATGGTGCCTCTGAGGAAAC	2358
Db	2221	GAGAACCTGTCTGGCTTCCCTCCCAAGGAGGATGAGATGGTGCCTCTGAGGAAAC	2280
Qy	2359	TATGTGCCCGTCACAGCTCCTCCAGTCCAACTGATGGCCAGATGTCACGAGGCGCAGAG	2418
Db	2281	TATGTGCCCGTCACAGCTCCTCCAGTCCAACTGATGGCCAGATGTCACGAGGCGCAGAG	2340
Qy	2419	GACAGCAGCAGGATCTTTCCAAACCACATCTGCTGGCTCT	2458
Db	2341	GACAGCAGCAGGATCTTTCCAAACCACATCTGCTGGCTCT	2380

RESULT 4

US-09-149-476-191

; Sequence 191, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: P2002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCI/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,600

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,502

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,633

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,583

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,617

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,618

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,503

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,592

; EARLIER FILING DATE: 1997-05-23

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; EARLIER FILING DATE: 1997-05-23



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3	EARLIER FILING DATE: 1997-08-22
4	EARLIER APPLICATION NUMBER: 60/056,894
5	EARLIER FILING DATE: 1997-08-22
6	EARLIER APPLICATION NUMBER: 60/056,911
7	EARLIER FILING DATE: 1997-08-22
8	EARLIER APPLICATION NUMBER: 60/056,636
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20	EARLIER APPLICATION NUMBER: 60/056,892
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24	EARLIER APPLICATION NUMBER: 60/047,595
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38	EARLIER APPLICATION NUMBER: 60/047,589
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42	EARLIER APPLICATION NUMBER: 60/047,614
43	EARLIER FILING DATE: 1997-05-23
44	EARLIER APPLICATION NUMBER: 60/043,578
45	EARLIER FILING DATE: 1997-04-11
46	EARLIER APPLICATION NUMBER: 60/043,576
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48	EARLIER APPLICATION NUMBER: 60/047,501
49	EARLIER FILING DATE: 1997-05-23
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56	EARLIER APPLICATION NUMBER: 60/056,862
57	EARLIER FILING DATE: 1997-08-22
58	EARLIER APPLICATION NUMBER: 60/056,881
59	EARLIER FILING DATE: 1997-08-22
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61	EARLIER FILING DATE: 1997-08-22
62	EARLIER APPLICATION NUMBER: 60/056,875
63	EARLIER FILING DATE: 1997-08-22
64	EARLIER APPLICATION NUMBER: 60/056,862
65	EARLIER FILING DATE: 1997-08-22
66	EARLIER APPLICATION NUMBER: 60/048,964
67	EARLIER FILING DATE: 1997-06-06
68	EARLIER APPLICATION NUMBER: 60/057,650
69	EARLIER FILING DATE: 1997-09-05

EARLIER APPLICATION NUMBER: 60/056,884  
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 EARLIER APPLICATION NUMBER: 60/057,669  
 EARLIER FILING DATE: 1997-09-05  
 EARLIER APPLICATION NUMBER: 60/049,610  
 EARLIER FILING DATE: 1997-06-13  
 EARLIER APPLICATION NUMBER: 60/061,060  
 EARLIER FILING DATE: 1997-10-02

Query Match 91.5%; Score 2259.2; DB 3; Length 2779;  
 Best Local Similarity 96.5%; Pred. No. 0;  
 Matches 2365; Conservative 10; Mismatches 5; Indels 70; Gaps 4;

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RESULT 5

US-09-149-476-314

; Sequence 314, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: P2002P1

; CURRENT APPLICATION NUMBER: US/09149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

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; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

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; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,502

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,633

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,583

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,617

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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
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; EARLIER APPLICATION NUMBER: 60/056,884
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; EARLIER APPLICATION NUMBER: 60/049,610
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; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      83.5%; Score 2061.8; DB 3; Length 2860;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 2364; Conservative 4; Mismatches 31; Indels 86; Gaps 20;

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2657 CAACTGATGCCCCAGATGACAGGAGGCCAGAGGAGGCCAGAGGACAGAGGATCTTTCCAAACA 2716  
2445 CATCTGCTGCTCTGGGTTCCAGT 2469  
2717 CATCTGCTGCTCTGGGTTCCAGT 2741

RESULT 6

US-09-484-970B-67  
; Sequence 67, Application US/09484970B  
; Patent No. 6426186  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Karen A.  
; APPLICANT: Volkman, Wayne  
; APPLICANT: Walker, Michael G.  
; TITLE OF INVENTION: BONE REMODELING GENES  
; FILE REFERENCE: PB-0014 US  
; CURRENT APPLICATION NUMBER: US/09/484,970B  
; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PERL Program  
; SEQ ID NO 67  
; LENGTH: 1790  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6426186 198309.5CB1  
; NAME/KEY: unsure  
; LOCATION: 1241-1260  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-484-970B-67

Query Match 69.7%; Score 1720; DB 3; Length 1790;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1731; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

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QY 719 TCAGTGGAGTACCCCTCTCTTTGGCCGCTTGACCAAGCAGTGGGATGTGGTAAGTACC 778
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QY 779 TCCTGGAGAACCCACACACAGCCCGCCAGCGTG - CAGGCCACTGACTCCAGGGCAACACA 837
Db 61 TCCTGGAGAACCCACACACAGCCCGCCAGCGTGCCAGGCCACTGACTCCAGGGCAACACA 120
QY 838 GTCTGTGATGCCCTAGTAGATCTCGGACAACTCAGCTGAGAACATTCACATGGTGACC 897
Db 121 GTCTGTGATGCCCTAGTAGATCTCGGACAACTCAGCTGAGAACATTCACATGGTGACC 180
QY 898 AGCATGTATCATGGGCTCTCAAGCTGGGGCCCGCTCTGCGCCCTACCGTGCAAGCTTGAG 957
Db 181 AGCATGTATCATGGGCTCTCTCAAGCTGGGGCCCGCTCTGCGCCCTACCGTGCAAGCTTGAG 240
QY 958 GACATCCGCAACTGCAAGATCTCAGCCCTCTGAAGCTGGCCGCCCAAGGAGGCAAGATC 1017
Db 241 GACATCCGCAACTGCAAGATCTCAGCCCTCTGAAGCTGGCCGCCCAAGGAGGCAAGATC 300
QY 1018 GAGATTTTACGGACATCTCGACGCGGAGTTTTCAGGACTGAGCCACCTTTCCCGAAG 1077
Db 301 GAGATTTTACGGACATCTCGACGCGGAGTTTTCAGGACTGAGCCACCTTTCCCGAAG 360
QY 1078 TTCACCGAGTGTGTATGGCCCTGTCGGGCTGTGCTGTATGACCTGGCTTCTGTGGAC 1137
Db 361 TTCACCGAGTGTGTATGGCCCTGTCGGGCTGTGCTGTATGACCTGGCTTCTGTGGAC 420
QY 1138 AGCTGTGAGGAGAACTCAGTGTGGAGATCAITGGCTTTCAITTCGAAGAGCCCGCAACCGA 1197
Db 421 AGCTGTGAGGAGAACTCAGTGTGGAGATCAITGGCTTTCAITTCGAAGAGCCCGCAACCGA 480
QY 1198 CACCGAATGTGTTTTGAGACCCCTGAAACAACTGCTGAGGCGAATGGGATCTGCTC 1257
Db 481 CACCGAATGTGTTTTGAGACCCCTGAAACAACTGCTGAGGCGAATGGGATCTGCTC 540
QY 1258 ATCCCAAGTCTCTTAAATCTCTGTGTAATCTGATCTACATGTTTCATCTTCACCGCT 1317
Db 541 ATCCCAAGTCTCTTAAATCTCTGTGTAATCTGATCTACATGTTTCATCTTCACCGCT 600
QY 1318 GTTGCTTACCATCAGCCTACCTTGAAGAAGCAGSCCGCCCTCACTGAAAGCGGAGGTT 1377
Db 601 GTTGCTTACCATCAGCCTACCTTGAAGAAGCAGSCCGCCCTCACTGAAAGCGGAGGTT 660
QY 1378 GGAATCTCAGTGTGTCAGCGGACCATCTTATCTGTAGGCGGATCTACCTCTC 1437
Db 661 GGAATCTCAGTGTGTCAGCGGACCATCTTATCTGTAGGCGGATCTACCTCTC 720
QY 1438 GTGGGCGAGTGTGTACTTCTGGCGGCGCCACGTTTCATCTGATCTCGTTCATAGAC 1497
Db 721 GTGGGCGAGTGTGTGTACTTCTGGCGGCGCCACGTTTCATCTGATCTCGTTCATAGAC 780
QY 1498 AGCTACTTTGAAATCTCTTCTCTGTTCAGGCGCTGCTCAGTGTGTGCCAGGTGCTG 1557
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QY 1558 TGTTCCTGGCCATCGAGTGTACTGCGCCCTGCTGTGTGTGCTGCTGCTGCTGCTGCTG 1617
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QY 1618 CTGAACTGCTTTACTATACAGTGGCTTCCAGACACAGGCATCTACAGTGTCTATGATC 1677
Db 901 CTGAACTGCTTTACTATACAGTGGCTTCCAGACACAGGCATCTACAGTGTCTATGATC 960
QY 1678 CAGAAGTCTATCTCGCGGACTGCTGCGCTTCTCTGATCTACTTAGTCTTCTCTTTTC 1737
Db 961 CAGAAGTCTATCTCGCGGACTGCTGCGCTTCTCTGATCTACTTAGTCTTCTCTTTTC 1020
QY 1738 GCTTCGCTGTAGCCCTGGTGTAGCTGTGAGCCAGAGGCTTGGCGCCCGCAAGCTCTTACA 1797
Db 1021 GCTTCGCTGTAGCCCTGGTGTAGCTGTGAGCCAGAGGCTTGGCGCCCGCAAGCTCTTACA 1080
QY 1798 GGCCCCAATGCCACAGATCTAGTGCAGCCCATGTGAGGACAGGAGGACAGGGCAACCGG 1857
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Db 1081 GGCCCCAATGCCACAGATCTAGTGCAGCCCATGGAGGACAGGAGCAACCGG 1140
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Db 1141 GCCCAGTACAGGGGTATCTCTGAAGCTCTCTTGGAGCTCTTCAAAATTCACCAATCGGCATG 1200
QY 1918 GGCGAGTCTGGCTTCCAGGAGCAGCTGCACTTCCGCGGATGGTGTCTGTCTGTGCTG 1977
Db 1201 GGCGAGTCTGGCTTCCAGGAGCAGCTGCACTTCCGCGGCAANNNNNNNNNNNNNN 1260
QY 1978 GCTTACGTCTGCTACCTACATCTCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAG 2037
Db 1261 GCTTACGTCTGCTACCTACATCTCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAG 1320
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Db 1321 ACCGTCAACAGTGTGCCACTGACAGCTGAGCATCTGGAAGCTGCAGAAAGCCATCTCT 1380
QY 2098 GTCTGGAGATGGAGAAATGGCTATTGGTGTGCAGAAAGCAGCGGGCAGGTGTGATG 2157
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QY 2278 GCAGGTGTCTCCGAACTCTCGAGAAACCTGTCTCTGGCTTCCCTCCCAAGGAGGATGAG 2337
Db 1561 GCAGGTGTCTCCGAACTCTCGAGAAACCTGTCTCTGGCTTCCCTCCCAAGGAGGATGAG 1620
QY 2338 GATGGTCTCTCAGGAAACTATATGTGCCGCTCCAGTCTCTCAGTCCAACTGATGGCCC 2397
Db 1621 GATGGTCTCTCAGGAAACTATATGTGCCGCTCCAGTCTCTCAGTCCAACTGATGGCCC 1680
QY 2398 AGATCAGCAGGAGGCGCAGGAGCAGAGAGATCTTTCCAAACCACTCTCTGTGGCTC 2457
Db 1681 AGATCAGCAGGAGGCGCAGGAGCAGAGAGATCTTTCCAAACCACTCTCTGTGGCTC 1740
QY 2458 TGGGGTCCCCAGT 2469
Db 1741 TGGGGTCCCCAGT 1752
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## RESULT 7

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US-09-235-451-3
; Sequence 3, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: R. rattus
; FEATURE:
US-09-235-451-3
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Query Match		61.7%;	Score 1522.4;	DB 3;	Length 2736;	
Best Local Similarity		78.9%;	Pred. No. 0;			
Matches 1935;		Conservative	0;	Mismatches 466;	Indels 53;	Gaps 8;
Qy	28	AGACAGGACCTTTGACATCTCCATCTGCACAGAGGTCCTGGCTGGACCGAGCAGCCTCCT	87			
Db	262	AGAGAGACCTTTAAACATCTCCATCTCTACAGAGGTTTCAGCTGTAGAGCATCTCCT	321			
Qy	88	CCTCTAGGATGACCTCACCTCCAGCTCTCCAGTTTTTCAGGTTGGAGACATTTAGATGA	147			
Db	322	-CTCTCAGGATGACTTCAGCTCCAGCCCTCCAGCTTCAGGCTGGAGACTTCGGATGA	380			
Qy	148	GGCCAGAGATGGCTCTGAGGCGGACAGAGGAAAGCTGGATTTTGGAGCGGGCTGCCT	207			
Db	381	GATGAAGAGGCAATGCTGAGGTGAACAAGGGGAAGCAGGA-----ACCGCCC	428			
Qy	208	CCCATGGAGTCACAGTTTCAGGGCGAGGACCGGAAATTCGCCCTCAGATAAGATCAAC	267			
Db	429	CCCATGGAGTCACATTCACAGGGAGGACCGGAAATTCCTCCCTCAGATCAAGTGAAC	488			
Qy	268	CTCAACTACCGAAGGGA-----ACAGGTGCCAGTCAGCCGGATCCAAAC	312			
Db	489	CTCAACTTCATAAAGAGACCTCTAAACACATCTCTGCTCCAGCCAGCAGGAGCCAGAT	548			
Qy	313	CGATTTGACCGAGATGGCTCTTCAATGCGGTCTCCGGGGTGTCCCGAGGATCTGGCT	372			
Db	549	CGGTTTTGACCGTGACCGACTCTTCAGTGTGGTCTCCCGGGGTGTCCCGAGGAACTGACT	608			
Qy	373	GGACTTCCAGATACCTGACCAAGACAGCAAGTACTCTCACCGACTCGGAATACACAGAG	432			
Db	609	GGACTGTAGAACTCTGCGCTGGAAACAGCAAGTACTCTACTGACTCTGCAACACAGAA	668			
Qy	433	GGCTCCACAGGTAAAGCTGCTGATGAAGGCTGTGCTGAACCTTAAAGACGGAGTCAAT	492			
Db	669	GGCTCCACTGGAAGAGCTGCTGATGAAGGCTGTGCTGAACCTTCAGGATGGGTCAAT	728			
Qy	493	GCCTGCATTCGCACTGCTGCAAGTCGACAGGAGCTCTGGGAAATCTCAGCCCCCTGTTA	552			
Db	729	GCCTGCATCATGCGCTGCTGCAGATTTGAACAGGATTCGCGCAATCCCAAGCCCCCTCGTC	788			
Qy	553	AATGCCAGTGACAGATGACTATTACCGAGGCGCACAGCGCTCTGCACATCGCCATTGAG	612			
Db	789	AATGCCAGTGCAACCGATGATTTCTACCAAGGCCACAGTGGCTGCACTCGCCATAGAG	848			
Qy	613	AAGAGGAGTCTGAGTGTGTGAAGCTCTCTGGTGGAGAAATGGGCCCAATGTGCATGCCCG	672			
Db	849	AAGAGGAGCTGCAGTGCGTGAAGCTGCTGCTAGAGAAATGGAGCGGATGTTCACTCCGA	908			
Qy	673	GCCTGGGCGCTTCTTCAGAAAGGGCCAAAGGAGCTTGTCTTTTATTTGGGTGAGCTACCC	732			
Db	909	GCCTGTGGCGCTTCTTCAAAGAGCACCAAGGAACTTGTTCATTTTGGAGAGCTACCT	968			
Qy	733	CTCTCTTGGCCGCTTGACCAAGCAGTGGGATGTGTAAAGCTACCTCTCGGAGAACCCCA	792			
Db	969	CTTCTCTGGCTGCTGCAACAGAGTGGGATGTGTGACCTTACCTCTCTCGGAGAACCCCA	1028			
Qy	793	CACCAGCCCGCAGCTTCAGGCGCACTGACTCCAGGGCGCAACAGTCTCTGCAATGCCCTA	852			
Db	1029	CACCAGCCCGCAGCTTCGAGGCGCCAGCTCCTCTGGGCAACAGTCTCTGCTGCTGCTG	1088			
Qy	853	GTGATGATCTCGGACAACTCAGCTGAGAAACATTTGCACTGTGTGACAGCATGTATATGGG	912			
Db	1089	GTAATGATTCAGATAACTCGCTCGTGAACAGTGTGCTGCTGATTCACATGTATACGACGG	1148			
Qy	913	CTCTCTCAAGCTGGGGCGGCTCTGCTGCTACCGTTCAGCTTCAGGACATCCGCAACCTG	972			
Db	1149	CTTCTCAAAATGGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1208			
Qy	973	CAGGATCTCAGGCTCTGAAGCTGGCGCGCAAGAGGCGAAGATCGAGATTTTCAGGCAAC	1032			
Db	1209	CAAGGCTTCACACCCCTGAAACTAGCGCGCAAGGAGGCAAAATCGAGATTTTCAGGCAAC	1268			
Qy	1033	ATCTCTGACGCGGAGTTTTTCAGGACTGAGCCA---CCTTTCCGAAAGTTCCACGAGTGG	1089			
Db	1269	ATCTCTGACGCGGAAATTTCTCAGGACCGTACGAGCCCTTTCCGAAAGTTTACTGAGTGG	1328			
Qy	1090	TGCTATGGGCCCTGTCCGGGTGTCTGTATGACCTCGGTCTCTGTGGACAGCTGTGTGAGGAG	1149			
Db	1329	TGTTACGGTCTGTGGGGTATCGCTGTACGACCTGTCTCTGTGGACAGCTGGGAAAG	1388			
Qy	1150	AACTCAGTGTCTGGAGATCATTCCTTTTCAATTCGAAGAGCCCGCACCGAACCAATGGTTC	1209			
Db	1389	AACTCGGTCTGGAGATCATTCGCTTTTCAATTCGAAGAGCCCGCACCGCACCGATGTGTG	1448			
Qy	1210	GTTTTGGAGCCCTGACAAACCTGTGCGAGGGGAAATGGGATCTGCTCATCCCAAGTTC	1269			
Db	1449	GTTTTAGAACCACTGAACAAGCTTCTGACAGGAGAAATGGGATCGGCTGCTCTCAAGATTC	1508			
Qy	1270	TTCTTAAACTTCTGTGTAAATCTGATCTACATGTTCATCTTTCACCGCTCTTTCCTACCAT	1329			
Db	1509	TTCTTCAACTTCGCTGTCTACTTGGTCTACATGTTTCACTTTCACCGCTCTTTCCTACCAT	1568			
Qy	1330	CAGCCTTACCTGAAAGAGCAGCGCCCTCTCACCTGAAAGCGGAGGTTTGGAAACTCCATG	1389			
Db	1569	CAGCCTTCCCTGGATCAGCCAGCCATCCCTCTCATCAAAAGCGACTTTTGGGGAATCCATG	1628			
Qy	1390	CTGCTGACGGGCGACATCTTATCTGTCTAGGGGGGATCTACTCTCTGCTGGGCCAGCTG	1449			
Db	1629	CTGCTGCTGGGCGACATCTGATCTCTGCTTGGGGGTATTTACTCTTACTTGGGCCAGCTG	1688			
Qy	1450	TGCTACTTCTGGCGGCGCACGTTGTTCACTCGATCTCTGTTTATCTGATCTCATTTGAGAA	1509			
Db	1689	TGCTACTTTTGGCGGCGCGCTGTTTATCTGATCTCATTTATGACAGCTACTTTTGA	1748			
Qy	1510	ATCTCTTCTCTGTTTCAGGCGCTCTGCTCACAGTGGTGTCCAGGTGCTGTGTTTCTGGCC	1569			
Db	1749	ATCTCTTCTCTGTTTCAGGCTCTGCTCACAGTGTGTCTCCAGGTGTGCTGCTTATGAG	1808			
Qy	1570	ATCGAGTGTACTCGCCCTGCTGTGTCTGCGCTGTGCTGCGCTGGCTGCGTGAACCTGCTT	1629			
Db	1809	ACTGAATGTACTCTACCTCTGCTGTGTATCCCTAGTGTATCCCTAGTGTGGCTGGAACCTGCTT	1868			
Qy	1630	TACTATACAGTGGCTTCCAGCACACAGGCATCTACAGTGTCTATGATCCAGAGGTCTATC	1689			
Db	1869	TACTACACAGGGCTTTTCAGCACACAGGCATCTACAGTGTCTATGATCCAGAGGTCTATC	1928			
Qy	1690	CTGGGAGCCTGCTGGCTTCTCTGATCTACTTATGCTTCTCTCTTCTGCTGCTGCTGTA	1749			
Db	1929	CTTCGAGACCTGCTCGCTTCTGCTGTCTACCTGCTTCTCTTCTGCTGCTTCTGCTGTA	1988			
Qy	1750	GCCCTGGTGGCTGAGCCAGGAGGCTTGGCGCCCGGAGCTCTTACAGSCCCCAATGCC	1809			
Db	1989	GCCCTAGTAAAGCTTGGAGAGAGGCGCGAAGTCCCAAGCCCCCTGAAGATTAACAACTCC	2048			
Qy	1810	ACAGAGTCAAGTTCAGCCCATGGAGGACAGAGGAGCAGGGGCAACGSGGCGCCAGTACAGG	1869			
Db	2049	ACAGTGAAGGACAGCCACGCTGGGCGGCGGAGGAGGAGGCG-----AGCTCATATCGG	2102			
Qy	1870	GGTATCTGGAAAGCCTCTCTGGAGCTCTTCAAATTCACCATCGGCAATGGGCGAGCTGGCC	1929			
Db	2103	AGCATCTGGATCGCTCTCTAGAGCTTTCAGATTTTCAACATTTGGTATGGGGAGCTGGCT	2162			
Qy	1930	TTCCAGGAGCAGCTGACATTCGCGCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1989			
Db	2163	TTCCAGGAAACGCTGGTTTTCTGGGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2222			
Qy	1990	CTCACCTCATCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACCGTCAACAGT	2049			
Db	2223	CTCACCTAGCTCTCTGCTCAACATGCTCATTTGCTCTCATGAGCGAAACTGTCAACACAC	2282			
Qy	2050	GTCCGCACTGACAGCTGGAGCATCTGGAAGCTGCGAAGAACCTCTCTCTCTCTGGAGATG	2109			
Db	2283	GTTCGCTGACCAACAGCTGGAGCATCTGGAAGTTTGCAGAAAGCCATCTCTCTCTTGGAGATG	2342			
Qy	2110	GAGAATGGCTATTGTTGGTGTG---AGGAAGAGCAGCGGGCAGGTGTGTGTGTGACCGT	2166			



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Db      2343 GAGATGGTACTTGGTGGTCCGAGGAGAAACATCGTGAAGGGAGGCTGCTGAAGATC 2402
Qy      2167 GGCACTAAGCCAGATGGCAGCCCGATGAGCGCTGGTGTCTTCAAGGTGAGGAGGTGAAC 2226
Db      2403 GGCACAGGGGGGATGGTACCCCTGATGAGCGCTGGTGTCTTCAAGGTGAGGAGGTGAAT 2462
Qy      2227 TGGGCTTCATGGGAGCAGCGCTGCCCTAGCTGTGTGAGGACCCGTCAGGGGAGGTGTC 2286
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Qy      2287 CCTCGAACTCTCGAGAACCCCTGCTCTGGCTTCCCTCCCAAGGAGGATGAGGATGGTGC 2346
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Qy      2347 TCTGAGGAAACATATGTGCCCGTCCAGCTCTCCAGTCCCACTGATGGCCAGATGAGC 2406
Db      2571 TCAGAGGAACACCTCTGCCCTTTCAGGCTCTCCAGTCTCCCTCCCTGATGGGCCAGATGAGC 2630
Qy      2407 AGGAGGCCAG-AGGACAGACAGAGGATCTTCCAACTCATCTGCTGGCTCTG 2459
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RESULT 8
US-09-978-303-3
; Sequence 3, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: R. rattus
US-09-978-303-3

Query Match      61.7%; Score 1522.4; DB 4; Length 2736;
Best Local Similarity 78.9%; Pred. No. 0;
Matches 1935; Conservative 0; Mismatches 466; Indels 53; Gaps 8;

Qy      28 AGACAGGACCTTGCATCTCCATCTGCACAGAGGTCTGGTGGACCGGAGCAGCTCCT 87
Db      262 AGAGAGGAACCTTAACATCTCCATCTCTACAGAGGTTTCAGCTGTAAGGAGCATCTCCT 321
Qy      88 CCTCTAGATGACTCCTACCTCCAGCTCTCCAGTCTTCCAGTTTGGAGACATTAGATGGA 147
Db      322 -CTCTCAGATGACTTTCAGCTCTCAGCCCCCAGCTTTCAGGCTGGAGACTTCCGATGGA 380
Qy      148 GSCCAAGAGATGGCTCTGAGCGGACACAGAGAAAGCTGGATTTTGGAGCGGCGTCCCT 207
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Qy      208 CCCATGAGTACAGTCTCAGGCGGAGGACCGGAAATTCGCCCTTCAGATGAAGTCAAC 267
Db      429 CCCATGAGTACCAATTCAGAGGAGGAGCGGAAATTCCTCCCTTCAGATCAAAAGTGAAC 488
Qy      268 CTCAACTACCGAAGGGA-----ACAGGTGCCAGTCCAGCCGGATCCAAAC 312

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Db      489 CTCAACTTCATAAAGAGACCTCTCTAAAAACACTTCTGTCTCCAGCCAGCAGGAGCCAGAT 548
Qy      313 CGATTTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCGGAGATCTGGCT 372
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Qy      433 GGCTCAGAGTTAAGCGTGCCTGATGAAGGCTGTCTGAACTTAAAGCCAGGATCAAT 492
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Qy      1033 ATCTCTCAGCGGGAGTTTTCAGGACTGAGGCA--CCTTTCCGAAAGTTTCACCGAGTGG 1089
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Db      1389 AACTCGGTGTGAGATCATCGCTTTTTCATTTGAGAGCGGCAAGTCCGACACCGAATGGT 1448
Qy      1210 GTTTTGGAGCGCTGTGAACAACTGCTGAGCGGAAATGGGATCTGCTCATCCCCCAAGTTC 1269
Db      1449 GTTTTGAACAACACTGAACAAGTCTTGCAGAGAAATGGGATCGGCTCGTCTCAAGATTC 1508
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Qy      1330 CAGCTTACCTTGAAGAGGAGCGGCGGCTCTCACTGAAAGCGGAGGTGTGAAATCTCATG 1389

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Db 1569 CAGCCTTCCCTGGATCAGCCAGCCATCCCTCATCAAAAGCGACTTTTGGGGATCCATG 1628  
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Db 1629 CTGCTGCTGGGCCACATCTGATCTCTGCTGGGGGTATTTACCTCTACTTGGGCCAGCTG 1688  
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Db 1749 ATCCTCTTCTCTCAGGGCTCTGCTCACAGTGTGTCCAGTGTGTGCGCTTCATGGAG 1808  
QY 1570 ATCAGTGTGTAACCTGCCCCCTGCTGTGTCTGCGCTGGTGTGGCTGGCTGAACTGCTT 1629  
Db 1809 ACTGAATGGTACCTACCCCTGCTAGTGTATCTCCCTAGTGTGCTGGCTGGCTGAACTGCTT 1868  
QY 1630 TACTATACAGTGTGCTTCAGACACAGGATCTACAGTGTCTATGATCCAGAGGTCTATC 1689  
Db 1869 TACTACACACGGGGCTTTCAGCACACAGGATCTACAGTGTCTATGATCCAGAGGTCTATC 1928  
QY 1690 CTGCGGACCTGCTGGCTTCTCTGATCTACTTACTGTCTCTTTCGGCTTTCGCTGTA 1749  
Db 1929 CTTTCGAGACCTGCTCGTTCCTGCTGCTGCTACTCTGCTTCTCTTTCGGCTTTCGCTGTA 1988  
QY 1750 GCCTCTGGTAGCTGAGCCAGGAGGCTTGGCCCCGGAAGCTCCTACAGCCCCCAATGCC 1809  
Db 1989 GCCTTAGTAGCTTGGAGAGAGGCCGGAAGTCCCAAGGCCCTGAAGATAACAACCTCC 2048  
QY 1810 ACAGATCAGTCAGCCCATGAGGACACAGGAGGACAGGGGCAAGGGGCCAGTACAGG 1869  
Db 2049 ACAGTACGGAACAGCCCCACGGTGGGCCAGGAGGAGGAGCC-----AGTCCATATCGG 2102  
QY 1870 GGTATCTGGAAGCTCTTGGAGCTCTTCAAAATTCACCATCGCATGGCGAGCTGGCC 1929  
Db 2103 AGCATTCGATGCTCTCCCTAGAGCTGTTCAAGTTTACCATTTGATGGGGAGCTGGCT 2162  
QY 1930 TTCCAGGAGCAGCTGCACTTCCCGGCAATGGTGTCTGTCTGTCTGCTGGCTTACGTGCTG 1989  
Db 2163 TTCCAGGAACAGCTGGCTTTTCTGGGGTGGTCTGTCTGTGTGTGGCTACGTCTT 2222  
QY 1990 CTACCTACATCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAGCCGTCACAGT 2049  
Db 2223 CTACCTACGCTCTGCTGCTCAACATGCTCATTTGCTCTCATGAGCGAAACTGTCAACCCAC 2282  
QY 2050 GTGCCACTGACAGCTGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGCTCTGGAGATG 2109  
Db 2283 GTTGTCTGACACAGCTGAGCATCTGGAGTTGGAGAGCCATCTCTGCTTGGAGATG 2342  
QY 2110 GAGAAATGGCTATTGGTGGTGC---AGGAAGACAGCGGGCAGGTGTGATGCTGACCGTT 2166  
Db 2343 GAGAAATGGTACTGGTGGTGGAGGAGAAACATCGTGAAGGGAGGCTGTCTGAAAGTC 2402  
QY 2167 GGCACCTAAGCCAGATGCGACCGCGATGAGCGCTGTGCTTCAAGGTGGAGGAGTGAAC 2226  
Db 2403 GGCACCGGGGGATGTTACCCCTGATGAGCGCTGTGCTTTCAGGGTGGAGGAGTAAAT 2462  
QY 2227 TGGGCTTCATGGAGACAGCGCTGCTACGCTGTGTGAGGACCCGTCAGGGCGAGGTGTC 2286  
Db 2463 TGGGCTGCTTGGGAGAGACTTCTCCACCTTATCTGAGGATCCATCAGGGCCAGGCATC 2522  
QY 2287 CCTCGAACTCTCGAGAAACCTGTCTGGCTTCCCTCCCAAGGAGGATAGGATGGTGC 2346  
Db 2523 ACTGGTAATAAAGAAACC-----CAACCTCTAAACGGGGGAAGAACAGTGC 2570  
QY 2347 TCTGAGGAACATATGTGCGCGTCCAGCTCTCTCCAGTCCAACTGATGGCCCAAGTCAGC 2406  
Db 2571 TCAGAGGAAGACCATCTGCCCCCTTTCAGGTCCTCCAGTCCCCCTGATGGCCCAAGTCAGC 2630  
QY 2407 AGGAGGCCAG-AGGACAGAGCAGAGGATCTTTCCAAACCATCTGCTGGGCTCTG 2459  
Db 2631 AGCAGGCTGCGAGGATGAGGTAGGGATCTTCCAGGCCACACAGAGGCTACTG 2684

RESULT 9  
US-09-235-451-22  
; Sequence 22, Application US/09235451  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: 9076/084CIP  
; CURRENT APPLICATION NUMBER: US/09/235,451  
; CURRENT FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/072,151  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 08/915,461  
; PRIOR FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 884  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)...(764)  
; OTHER INFORMATION: Human VR2 cDNA  
US-09-235-451-22

Query Match 30.4%; Score 750.8; DB 3; Length 884;  
Best Local Similarity 92.0%; Pred. No. 4.9e-180;  
Matches 839; Conservative 3; Mismatches 0; Indels 70; Gaps 2;  
QY 1558 TGTTCCTGGCCATCGAGTGTGTACCTGCCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1617  
Db 1 TGTTCCTGGCCATCGAGTGTGTACCTGCCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 60  
QY 1618 CTGAACCTGCTTTTACTATACAGTGGCTTCCAGCACACAGGCACTTACAGTGTATGATC 1677  
Db 61 CTGAACCTGCTTTTACTATACAGTGGCTTCCAGCACACAGGCACTTACAGTGTATGATC 120  
QY 1678 CAGAAGTTCATCTCTGGGACCTGTGCGCTTCTCTGATCTACTTACTTCTTCTTTC 1737  
Db 121 CAGA----- 124  
QY 1738 GGTTCGCTGTAGCCCTGTGAGCCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCCTACA 1797  
Db 125 -----AGCCCTGTGAGCCTGAGCCAGGA---TTGGGGCCCCGAGCTCCTACA 170  
QY 1798 GGGCCCCAATGCCACAGAGTCACTGACGCCCATGAGAGGACAGAGGACAGAGGCAACGGG 1857  
Db 171 GGGCCCCAATGCCACAGAGTCACTGACGCCCATGAGAGGACAGAGGACAGAGGCAACGGG 230  
QY 1858 GGGCAGTACAGGGGTATCTCGAAGCCTCTTGGAGCTCTTCAAAATTCACCATCGGCATG 1917  
Db 231 GGGCAGTACAGGGGTATCTCGAAGCCTCTTGGAGCTCTTCAAAATTCACCATCGGCATG 290  
QY 1918 GGGCAGTGGCTTCCAGGAGCAGTGTGCACTTCCCGCGCATGCTGTGCTGTGCTGTGCTG 1977  
Db 291 GGGCAGTGGCTTCCAGGAGCAGTGTGCACTTCCCGCGCATGCTGTGCTGTGCTGTGCTGCTG 350  
QY 1978 GCTACGCTGCTCACTCACTATCTGCTGTGCTCAACATGCTCATTCGCCCTCATAGAGGAG 2037  
Db 351 GCTACGCTGCTGCTCACTCACTATCTGCTGTCTCAACATGCTCATTCGCCCTCATAGAGGAG 410  
QY 2038 ACCGTCAAAGTGTGCCCATGACAGCTGAGCATCTGGAAGCTGGAAGCTGAGAAAGCACTCT 2097  
Db 411 ACCGTCAAAGTGTGCCCATGACAGCTGAGCATCTGGAAGCTGGAAGCTGAGAAAGCACTCT 470  
QY 2098 GTCTCTGGAGATGGAAATGGCTATTGGTGTGTCAGGAAGAGCAGCGGGCAGGTGTGATG 2157

Db 471 GTCTGGAGATGGGAATGGCTATTGGTGGTGCAGGAAGACGCGGCGAGGTGTGATG 530  
Qy 2158 CTGACCGTTGGCACTTAAGCCAGATGACCGCCGGATGAGCGCTGTGCTTCAAGGTGGAG 2217  
Db 531 CTGACCGTTGGCACTTAAGCCAGATGAGCGCCGGATGAGCGCTGTGCTTCAAGGTGGAG 590  
Qy 2218 GAGGTGAACCTGGGCTTTCATGGGAGCAGAGCTGCTCCCTACGCTGTGTGAGGACCCGCTCAGGG 2277  
Db 591 GAGGTGAACCTGGGCTTTCATGGGAGCAGAGCTGCTCCCTACGCTGTGTGAGGACCCGCTCAGGG 650  
Qy 2278 GCAGGTGCTCCTCGAACTCTCGAGAACCTGTGCTGTGCTTCCCTCCCAAGGAGGATGAG 2337  
Db 651 GCAGGTGCTCCTCGAACTCTCGAGAACCTGTGCTGTGCTTCCCTCCCAAGGAGGATGAG 710  
Qy 2338 GATGGTGCCTCTGAGGAAATATGTGCCGTCCAGCTCCTCAGTCCCACTGATGGCCC 2397  
Db 711 GATGGTGCCTCTGAGGAAATATGTGCCGTCCAGCTCCTCAGTCCCACTGATGGCCC 770  
Qy 2398 AGATGACGAGGAGGCCAGAGGACAGAGCAGAGGATCTTTCCAAACCACTCTGCTGGCTC 2457  
Db 771 AGATGACGAGGAGGCCAGAGGACAGAGCAGAGGATCTTTCCAAACCACTCTGCTGGCTC 830  
Qy 2458 TGGGGTCCCAGT 2469  
Db 831 TGGGGTCCCAGT 842

## RESULT 10

US-09-978-303-22  
; Sequence 22, Application US/09978303  
; Patent No. 6790629  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: Nucleic acid sequences encoding  
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related  
; TITLE OF INVENTION: polypeptides and uses thereof  
; FILE REFERENCE: UCAL084CON  
; CURRENT APPLICATION NUMBER: US/09/978,303  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/235,451  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/072,151  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 08/915,461  
; PRIOR FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 884  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-978-303-22

Query Match 30.4%; Score 750.8; DB 4; Length 884;  
Best Local Similarity 92.0%; Pred. No. 4.9e-180;  
Matches 839; Conservative 3; Mismatches 0; Indels 70; Gaps 2;  
Qy 1558 TGTTTCTGGCCATCGAGTGGTACTGCTCCCTGCTGTGTGCTGGCTGGTGGCTGG 1617  
Db 1 TGTTTCTGGCCATCGAGTGGTACTGCTCCCTGCTGTGTGCTGGCTGGTGGCTGG 60  
Qy 1618 CTGAACCTGCTTTACTATACACGTGGCTTCCAGACACAGGATCTACAGTGTATGTC 1677  
Db 61 CTGAACCTGCTTTACTATACACGTGGCTTCCAGACACAGGATCTACAGTGTATGTC 120  
Qy 1678 CAGAAGTTCATCTCTGGGACCTGCTGGCTTCTCTGATCTACTAGTCTCTCTTC 1737  
Db 121 CAGA----- 124  
Qy 1738 GGCTTCGCTGTAGCCCTGGTGGAGCTTGAGCCAGGAGGCTTGGCGCCCGGAGCTCTTACA 1797

Db 125 -----AGCCCTGGTGGAGCCTGAGCCAGGA---TTGGCGCCCCCGAGCTCCTACA 170  
Qy 1798 GGCCCCCAATGCCACAGAGTCACTGAGCCCATATGGAGGACAGAGGACGAGGCAACGGG 1857  
Db 171 GGCCCCCAATGCCACAGAGTCACTGAGCCCATATGGAGGACAGAGGACGAGGCAACGGG 230  
Qy 1858 GCGGAGTACAGGGGTATCTTGAAGCCTCTTTGGAGCTTTCAAAATTCACCATCGGATG 1917  
Db 231 GCGGAGTACAGGGGTATCTTGGWAGCCTCTTTGGAGCTTTCAAAATTCACCATCGGATG 290  
Qy 1918 GCGGAGTGGCTTCCAGGAGCAGCTTCCCGGGCATGCTGCTGCTGCTGCTGCTGCTG 1977  
Db 291 GCGGAGTGGCTTCCAGGAGCAGCTTCCCGGGCATGCTGCTGCTGCTGCTGCTGCTG 350  
Qy 1978 GCTTACGCTGCTGCTACCTACATCTCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAG 2037  
Db 351 GCTTACGCTGCTGCTACCTACATCTCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAG 410  
Qy 2038 ACCGTCAACAGTGTGCGCCACTGACAGCTGAGAGCATCTGGAAGCTGCAGAAAGCCATCTCT 2097  
Db 411 ACCGTCAACAGTGTGCGCCACTGACAGCTGAGAGCATCTGGAAGCTGCAGAAAGCCATCTCT 470  
Qy 2098 GTCTTGGAGATGGAGAAATGGCTATTGGTGGTGCAGGAAGACGCGGCGAGGTGTGATG 2157  
Db 471 GTCTTGGAGATGGAGAAATGGCTATTGGTGGTGCAGGAAGACGCGGCGAGGTGTGATG 530  
Qy 2158 CTGACCGTTGGCACTTAAGCCAGATGCGCCCGATGAGCGCTGTGCTTTCAGGGTGGAG 2217  
Db 531 CTGACCGTTGGCACTTAAGCCAGATGCGCCCGATGAGCGCTGTGCTTTCAGGGTGGAG 590  
Qy 2218 GAGGTGAACCTGGGCTTTCATGGGAGCAGAGCTGCTCCCTACGCTGTGTGAGGACCCGCTCAGGG 2277  
Db 591 GAGGTGAACCTGGGCTTTCATGGGAGCAGAGCTGCTCCCTACGCTGTGTGAGGACCCGCTCAGGG 650  
Qy 2278 GCAGGTGCTCCTCGAACTCTCGAGAACCTGTGCTGCTTCCCTCCCAAGGAGGATGAG 2337  
Db 651 GCAGGTGCTCCTCGAACTCTCGAGAACCTGTGCTGCTTCCCTCCCAAGGAGGATGAG 710  
Qy 2338 GATGGTGCCTCTGAGGAAATATGTGCCGTCCAGCTCCAGTCTCCAGTCCAACTGATGGCCC 2397  
Db 711 GATGGTGCCTCTGAGGAAATATGTGCCGTCCAGTCTCCAGTCTCCAACTGATGGCCC 770  
Qy 2398 AGATGACGAGGAGGCCAGAGGACAGAGCAGAGGATCTTTCCAAACCACTCTGCTGGCTC 2457  
Db 771 AGATGACGAGGAGGCCAGAGGACAGAGCAGAGGATCTTTCCAAACCACTCTGCTGGCTC 830  
Qy 2458 TGGGGTCCCAGT 2469  
Db 831 TGGGGTCCCAGT 842

## RESULT 11

US-09-149-476-315  
; Sequence 315, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07

[illegible]





Db 730 ACATCCCTGCTCTGAGATCGCGGCAACCGACAGCTTGAAGGCTTGTCAAC 789  
 QY 556 GCCAGTGCACAGATGATATTAACGAGGCAACAGCGCTCTGCAATCGCCATTTGAGAAG 615  
 Db 790 GCCAGCTACAGGACAGCTACTACAAGGGCCAGACAGCACTGCAATCGCCATCGAGAGA 849  
 QY 616 AGAGTCTGAGTGTGTGAGCTCTGTTGGAGATGGGGCCAAATGTGATGCCCGGCC 675  
 Db 850 CGCAACATGCGCTGTGTGAGCTCTGTTGGAGAACGGAGCAGACGTCCAGGCTCGCGCC 909  
 QY 676 TGGCGCGCTTCTTCAGAGGCGCAAG---GGACTTGTCTTTATTTTCGGTGAAGTACCC 732  
 Db 910 CATGGGACTTCTTTAAGAAACCAAGGGCGCTGGAATCTTACTTGGTGAATGCC 969  
 QY 733 CTCTCTTGGCGCTTGCACCAAGCAGTGGATGTGTGAAGTACTCTCTGGAGAACCCA 792  
 Db 970 CTGTCTGCGCGCTGCAACACAGCTGGGCACTCGTGAAGTCTCTGTGCAAGACTCC 1029  
 QY 793 CACAGCGCCGAGCTGAGGCACTGACTCCAGGGCAACAGTCTCTGATGCCCTA 852  
 Db 1030 TGGCAGACGGCCGACATCAGCGCGAGGACTCGTGGGCAACCGTGTGCAAGCGCTG 1089  
 QY 853 GTGATGATCTCGACAACTCAGCTGAGAACATTTGCACTGTGTGACCAAGCATGTATGGG 912  
 Db 1090 GTGAGTGGCGGACAAACAGCGCGCAACAGAGTTTGTGAGGAGCATGTACATGAG 1149  
 QY 913 CTCTCTCAAGCTGGGGCCGCTCTGCTGACCGTGTGAGTGTGAGGACATTCGCAACCTG 972  
 Db 1150 ATTCTGATGTGGGGCCAACTGCACCGCTGAACTGAGGAGGAGCTTCAACCAAG 1209  
 QY 973 CAGATCTCAGCTCTGAGCTGGCGCCAGAGGGGCAAGATCGAGATTTTCAGGCAC 1032  
 Db 1210 AAGGGAATGACGCGCTGGCTCTGGCAGCTGGGACCGGGAAGATTCGGGCTT 1269  
 QY 1033 ATCTGTCAGCGGAGTT-----TTCAAGACTGAGCCACCTTTCCCGAAAGTTCAACCGAG 1086  
 Db 1270 ATCTCAGCGGAGATTCAGAGGACCGAGTGCAGGACCTGTGCCAGAGTTTCAGGCAG 1329  
 QY 1087 TGTGTCTATGGCGCTCTCGGGTGTCTGTATGACTGTGCTTCTGTGGACAGCTGTGAG 1146  
 Db 1330 TGGGCTTACGGCGCGTGCACTCTGCTGTATGACCTGTCTGATCGACATCGACACCTCGGAG 1389  
 QY 1147 GAGAACTCAGTGTGAGATCATTTGCTTTTCAATTGCA---AGAGCCCGCACGACACCGA 1203  
 Db 1390 AAGAACTCGTGTGAGGATCGCCTTACAGCAGCAGCGAGACCCCTTAATCGCCACGAC 1449  
 QY 1204 ATGCTGCTTTTGGAGCCCTGAAACAACTGTGTCAGGCGAAATGGGA---TCTGCTCATC 1260  
 Db 1450 ATGCTCTTGGTGGAGCCGCTGAACCGACTCTGTCAGCAAGTGGGACAGATTCGTCAAG 1509  
 QY 1261 CCCAAGTTCTTTAAACTTCTCTGTAACTGTATCTACATGTTTCATCTTCAACGCTGTT 1320  
 Db 1510 CGCATCTTCTACTTCACTTCTGTCTACTGTCTGCTGTACATGATCATCTTCAACATGGCT 1569  
 QY 1321 GCCTACCATCAGCTTACCTGAAGAGCAGGCGCCCTCACCTGAAGCGGAGTTGGA 1380  
 Db 1570 GCCTACTACAGGCC-----CGTGGATGGCTTGGCTCTCTTAAAGTGGAAAAAATTGGA 1623  
 QY 1381 AACTCCATGCTGTGAGGGCCACATCTTATCTGCTAGGGGGATCTACTCTCTGCTG 1440  
 Db 1624 GACTATTTCCAGTACTTGGAGAGATCTGTCTGTGTTAGAGAGTCTACTTCTTTTTC 1683  
 QY 1441 GCGCAGCTGTGTACTTCTGCGGCGCAACGTGTTCATCTGATCTCGTTTCATAGACAGC 1500  
 Db 1684 CGAGGATTCAGTATTTCTTCAGAGGCGCGCTCGATGAAGACCTGTTGTGTGACAGC 1743  
 QY 1501 TACTTTGAATCTCTTCTGTTCCAGGCCCTGTCTACAGTGGTGTCCAGTCTGTGT 1560  
 Db 1744 TACAGTGAAGTCTTTCTTTCTGCACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1803  
 QY 1561 TTCTGCGCATCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620

Db 1804 TTCAAGCCACTCAAGAGGATATGTGGCTTCCATGGTATTCTCCCTGGCCTTGGGCTGGACC 1863  
 QY 1621 AACCTGCTTTACTATACAGCTGGCTTCCAGACACAGGCACTACAGTGTCTATGATCCAG 1680  
 Db 1864 AACATGCTCTACTACACCGCGGTTTCCAGAGATGGGCACTATATGCCGCTCATGATAGAG 1923  
 QY 1681 AAGGTCACTCTCGGAGCCTGTGCGCTTCTTCTGATCTACTAGTCTTCTTTTTCGGC 1740  
 Db 1924 AAGATGATCTCGAGAGACCTGTGCGGTTTTCATGTTTGTCTACATCTCTTCTTGTTCGGG 1983  
 QY 1741 TTCGCTGTAGCCTGTGTAGCCTGAGCAGGAGGCTTGGGCGCCCAAGCTCTCAAGGC 1800  
 Db 1984 TTTTCCACAGCGGTGTGTGACGCTGATTGAAGACGGGAAGATGACTCCCTGCGCTGAG 2043  
 QY 1801 CCCAATGCCACAGAGTCACTGTCAGGCCCATGAGGGGACAGAGGACGAGGCAACGGGGCC 1860  
 Db 2044 TCACGCTC-----GCACAGGTGCGGGGCTTGCCTGCGAGGCCCCCGATAGC 2091  
 QY 1861 CAGTACAGGGGTATCTCGAAGCCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGGC 1920  
 Db 2092 TCTTCAACACAGCTGTACTCCACCTGCTGGAGCTGTTCAAGTTTCAACATCGGCATGGGC 2151  
 QY 1921 GAGTGGCCTTCCAGAGCAGCTGACTTTCGCGGCACTGGTGTGCTGCTGCTGCTGCGCC 1980  
 Db 2152 GACCTGGAGTTCACTGAGAACTATGACTTCAAGGCTGTCTTCAATCTCTGCTGCTGCGCC 2211  
 QY 1981 TAGGTCTGCTCACCTTACATCTGCTGCTCAACATGCTATCGCCCTCATGAGCGAGACC 2040  
 Db 2212 TATGTAATTTCTACCTTACATCTCTCTGCTCAACATGCTATCGCCCTCATGSGTGAGACT 2271  
 QY 2041 GTCAACAGTGTGCCACTGACAGCTGAGCATCTGGAAGCTGCAAGAACCATCTCTGTCT 2100  
 Db 2272 GTCAACAGATCGCACAGAGAGCAAGAACATCTGGAAGCTGCAAGAGCCATCACCATC 2331  
 QY 2101 CTGAGATGAGAAATGGCTATGCTGTGTCGTCAGGAAGAG---CAGGGGCGAGTGTGATG 2157  
 Db 2332 CTGCAACGCGAAGAGCTTCTTAAAGTGCATGAGGAAGGCTTTCGCTCAGGCAAGCTG 2391  
 QY 2158 CTGACGCTTGGCACTAAGCCAGATGCGAGCCCGATGAGCGCTGCTGCTTCAAGGTTGGAG 2217  
 Db 2392 CTGAGGTGGGTACACACTGATGCGAAGGACGACTACCGTGTGTGCTTTCAGGGTGGAC 2451  
 QY 2218 GAGTGAACCTGGGCTTTCATGGGAGCAGACGCTGCTGCTGCTGCTGCTGAGGACCCG 2271  
 Db 2452 GAGTGAACCTGGACCACTGGAACACCAACGCTGGGATCATCAACGAAGACCCG 2505

RESULT 14

US-09-235-451-33  
 ; Sequence 33. Application US/09235451  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Julius, David J.  
 ; APPLICANT: Caterina, Michael J.  
 ; APPLICANT: Brake, Anthony J.  
 ; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
 ; CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
 ; POLYPEPTIDES AND USES THEREOF  
 ; FILE REFERENCE: 9076/084CIP  
 ; CURRENT APPLICATION NUMBER: US/09/235,451  
 ; CURRENT FILING DATE: 1999-01-22  
 ; PRIOR APPLICATION NUMBER: 60/072,151  
 ; PRIOR FILING DATE: 1998-01-22  
 ; PRIOR APPLICATION NUMBER: 08/915,461  
 ; PRIOR FILING DATE: 1997-08-20  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 33  
 ; LENGTH: 2544  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (14)...(2530)



; OTHER INFORMATION: Human VRI  
US-09-235-451-33

Query Match 26.8%; Score 660.8; DB 3; Length 2544;  
Best Local Similarity 61.1%; Pred. No. 4.8e-157;  
Matches 1206; Conservative 0; Mismatches 732; Indels 36; Gaps 7;

QY 316 TTTGACGAGATCGGCTCTTTCAATGCGGTCTCCGGGGTGTCCCGAGGATCTGGCTGGA 375  
DB 350 TATGATCGCAGGAGTATCTTTGAAGCGTGTCTCAGAAATACTGCCAGGATCTGGAGAGC 409  
QY 376 CTTTCCAGAGTACCTGAGCAGAGCAGCAAGTACTCACCGACTCGGATACACAGAGGGC 435  
DB 410 CTGCTGCTTCTCTGCAGAGAGCAAGACCTCACAGAACAGAGTTCAAGACCTT 469  
QY 436 TCCACAGGTAAGACGTGCTGTGTAAGAGCTGTCTGAACCTTAAGACGCGAGTCAATGCC 495  
DB 470 GAGCAGGGAAGACCTGTCTGCTGAAAGCCATGCTCNACTGACGACGACAGACACC 529  
QY 496 TGCATTCTGCACTGTCTGAGATCGACAGGGAATCTGGGCAATCTCAGCCCCCTGGTAAT 555  
DB 530 ACCATCCCCCTGCTCTCTGAGATCGCGCGCAACGACAGCCTGAAGGAGCTTGTCAAC 589  
QY 556 GCCAGTGCACAGTACTATTACCGAGGCCACAGCGCTCTGCACATCGCCATTGAGAG 615  
DB 590 GCCAGCTACACGACAGCTACTACAAGGGCCACAGCAGCTGCACATCGCCATCGAGAGA 649  
QY 616 AGGAGTCTGCAGTGTGTGAAGCTCTCTGTGGAGAAATGGGGCCAAATGTGCATGCCCGGCC 675  
DB 650 CGCNAATGGCCCTGGTGACCTCTCTGGTGGAGAACGGAGCAGACGTCCAGGCTGGGCC 709  
QY 676 TGGCGCGCTTTTCCAGAAAGGCGCAAG---GACATTGCTTTTATTGCGTGAGCTACCC 732  
DB 710 CATGGGAGCTCTTTAAGAAACCAAAGGCGCGCTGGATTCTACTTCGGTGAATGCC 769  
QY 733 CTCTCTTTGGCGCTTGCACCAAGCAGTGGATGTGGTAAGCTACCTCTCGGAGAACCCA 792  
DB 770 CTGTCTGCGCGCTGTCACCAACAGCTGGGATCGTGAAGTTCCTGCTGCGAGAACTCC 829  
QY 793 CACGAGCCCGCAGCTGCGAGGCACTGACTCCAGGGCAACACAGTCTCTGCATGCCCCA 852  
DB 830 TGGCAGAGCGCGACATCAGCGCCAGGACTCGGTGGGCAACACGGTGTGTCAGCGCTG 889  
QY 853 GTGATGATCTCGACAACTCAGCTGAGAAATTTGCACTGGTGAACGAGCATGTATGATGG 912  
DB 890 GTGGAGGTGGCCGACAAACAGCGCCGCAACACAGAAATTTGTGACGAGCATGTACAATG 949  
QY 913 CTCTCCAAAGCTGGGGCCGCTCTGCTGCTACCGTTCAGCTTGCAGCATCCGCAACCTG 972  
DB 950 ATTCTGATCTGGGGGCAAACTGCACCCGACGCTGAGCTGGAGGAGCTCACCAACAG 1009  
QY 973 CAGGATCTCAGCTCTGAAAGCTGGCGCGCAAGAGGGCAAGATCGAGATTTTCAGGCAC 1032  
DB 1010 AAGGGAATGACCGCTGCTGGCAGCTGGGACCGGGAAGATCGGGTCTTTGGCTAT 1069  
QY 1033 ATCTGAGCGGGAGTT-----TTGAGACTGAGCACTTTTCCCGAAGTTTCAAGG 1086  
DB 1070 ATTTCTCAGCGGGAGATCCAGGAGCCGAGTGCAGGCACCTGTCCAGGAAGTTTCAAG 1129  
QY 1087 TGTGCTATGCGCTGTCCGGGTGTGCTGTATGACTGTGCTGTGAGACAGCTGTGAG 1146  
DB 1130 TGGGCTTACGGGCGCGTGCATCTCTCTGTATGACCTGTCTGCTGCTGCTGAGACCTGG 1189  
QY 1147 GAGAACTCAGTGTGGAGATCATTTGCCCTTTTCAATTGCA---AGAGCCCGCACCGACCCGA 1203  
DB 1190 AAGAACTCGTGTGGAGGTGATCGCTACAGCAGCAGCGAGACCCCTTAATCGCCAGCAG 1249  
QY 1204 ATGGTCTTTTGGAGCCCTTGAAACAATCTGCTGAGCGCGAAATGGGA---TCTGCTCATC 1260  
DB 1250 ATGCTCTTGTGTGAGCGCGTGAACCGGACTCTCTGAGGACAAAGTGGGACAGATTCGTAAG 1309  
QY 1261 CCCAAGTCTCTTAAACTTCTGTGTAACTGTATCTGATCTACATGTTTCACTTCCAGCTGTT 1320

DB 1310 CGCATCTTCTACTTCACTTCTGCTGCTACTGCTGCTGATCATCATCTTCCACATGGCT 1369  
QY 1321 GCCTACCAATACCTTACCTTGAAGAGCAGCGCGCCCTCACTGTAAAGCGGAGGTTGGA 1380  
DB 1370 GCCTACTACAGGCC-----CGTGATGGCTTGGCTCCCTTTAAGATGAAAAAATGGA 1423  
QY 1381 AACTCCATGCTGCTGACGGCCACACTTATCTCTGCTAGGGGGGATCTACCTCTCTCGT 1440  
DB 1424 GACTATTTCCGAGTTACTTGGAGAGATCTGTCTGTGTTAGGAGGAGTCTACTTTCTTTTC 1483  
QY 1441 GGCAGCTGTGCTACTTCTGCGCGGCCACAGTGTTCATCTGGATCTCTGTTCTATAGACG 1500  
DB 1484 CGAGGATTCAGTATTTCTGCGAGAGCGCGCTCGATGAAGACCTGTTTGGAGACG 1543  
QY 1501 TACTTTGAATCCTCTTCTGTTTCAGGCCCTCTGCTCAAGTGGTGTCCAGGTTCTGTGT 1560  
DB 1544 TACAGTGAGATGCTTTCTTCTGCTGAGTCACTGTTTCTGCTGCGCCACCGCTGCTGTAC 1603  
QY 1561 TTTCTGGCCATCAGTGTGTACCTGCGCCCTGCTGTGCTGCTGCTGCTGCTGCTGCTG 1620  
DB 1604 TTACGCCACTCAAGAGATATGTGGCTTCCATGGTATTTCTCCCTGGCCTTGGGCTGGACC 1663  
QY 1621 AACCTGCTTTTACTATACAGTGGCTTTCAGACACACAGGCACTCTACAGTGTCTATGATCCAG 1680  
DB 1664 AACATGCTCTACTACACCGCGGTTTCCAGCAGATGGGCACTCTATGCCGTCTATGATAG 1723  
QY 1681 AAGGTCAATCCTCGGGAACCTGCTGGCTTCTTCTGATCTAATTAGTCTTCTTTTTCGGC 1740  
DB 1724 AAGATGATCCTGAGAGACCTGCGCGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1783  
QY 1741 TTTGCTGTAGCCCTGGTGAGCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCTACAGGC 1800  
DB 1784 TTTTCCACAGCGGTGGTGAGCTGATTTGAAGACGGAAGATGACTCTCCCTGCGCTGAG 1843  
QY 1801 CCCAATGCCACAGAGTCACTGTCAGCGCCATGAGGAGGACAGAGGACGAGGCAACGCGGCC 1860  
DB 1844 TCCACGTC-----GCACAGGTGCGGGGCTGCTGCGAGGCCCGCCGATAGC 1891  
QY 1861 CAGTACAGGGGTATCTCGAAAGCTTCTTTGAGAGCTTCTCAAAATTTCAACATTCGGCATGGGC 1920  
DB 1892 TCTTACACAGCGCTGTACTTCCACCTGCTGAGAGCTGTTCAAGTTTCAACATTCGGCATGGGC 1951  
QY 1921 GAGTGGCTTCCAGAGCAGCTGCACTTTCGCGGATGCTGCTGCTGCTGCTGCTGCTGCTG 1980  
DB 1952 GACCTGGAGTCTCAGAGAACTATGACTTCAAGGCTGTCTTCAATCACTGCTGCTGCTGCTG 2011  
QY 1981 TAGCTGCTCTCACTTACATCTCTGCTGCTCAACATGCTCATCGCCCTCATGAGCAGAGACC 2040  
DB 2012 TATGTAATTTCTACCTTACATCTCTGCTCAACATGCTCATCGCCCTCATGAGTGGAGACT 2071  
QY 2041 GTCAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGAGAAAGCCATCTCTGTC 2100  
DB 2072 GTCAACAGATGCGCAGAGAGCAGAAACATCTGGAAGCTGAGAGAGCCATCACCATC 2131  
QY 2101 CTGGAGATGAGAAATGGCTATTGGTGTGTCAGGAAGAAG---CAGCGGCGAGGTGTGATG 2157  
DB 2132 CTGACACGGAAGAGCTTCTTAAATGATGATGAGGAAGCCCTTCCGCTCAGGCAAGCTG 2191  
QY 2158 CTGACCGTTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGTGTGCTTTCAGGGTGGAG 2217  
DB 2192 CTGCGAGTGGGTACACACTGATGGAAGGAGCTACCGGTGGTGTCTTTCAGGGTGGAC 2251  
QY 2218 GAGGTGAATCGGCTTTCAGGAGCAGCTGCTGCTACGCTGTGTGAGGACCGG 2271  
DB 2252 GAGGTGAATCGGACCACTGGAAACCAACGCTGGGCACTCATCAACGAAGACCGG 2305

RESULT 15  
US-09-978-303-33  
; Sequence 33, Application US/09978303  
; Patent No. 6790629  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.



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; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaisin receptor and capsaisin receptor-related
; FILE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-978-303-33

Query Match      26.8%; Score 660.8; DB 4; Length 2544;
Best Local Similarity 61.1%; Pred. No. 4.8e-157;
Matches 1206; Conservative 0; Mismatches 732; Indels 36; Gaps 7;

Qy 316 TTTGACCGAGATCGGCTCTTCAATGCGGTCTCCGGGGTGTCCCGAGGATCTGGCTGGA 375
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 350 TATGATCGCAGGAGTATCTTTGAAGCGTGTCTCAGAAATACTGCCAGGATCTGGAGAGC 409
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 376 CTTCCAGAGTACCTGAGCAAGCAGCAAGTACTCTACCGACTCGGAATACACAGAGGGC 435
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 410 CTGCTGCTCTTCTCGAGAGAGCAAGACACTCTACAGACACGAGTTCAAGACCCCT 469
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 436 TCCACAGGTAAAGCTGCTGATGAAGCTGTGTGTAACCTTAAGGACGAGTCAATGCC 495
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 470 GAGACGGGAGACCTGTCTGCTGAAAGCCATGCTCAACCTGACAGCAGCAGACACACC 529
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 496 TGCATCTGCCATGCTGCGAGATCGACAGGAGCTCTGGGCAATCTCTAGCCCCCTGGTAAAT 555
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 530 ACCATCCCTCTGCTCTCTGAGATCGCGCGCAACCGGACACCTTGAAGGAGCTTGTCAAC 589
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 556 GCCAGGTGACAGATGACTATTACGAGGCCACAGCGCTCTGACATCTGCCATTGAGAAG 615
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 590 GCCAGTACAGGACGACTACTACAGGCCACAGACACTGACATCTGCCATCGCCATCGAGA 649
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 616 AGGAGTCTGCAGTGTGTGAAGCTCTCTGTGGAGAAATGGGCCAATGTGCATGCCCGGCC 675
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 650 CGCAACATGCCCTGGTGACCTCTCTGTGGAGAACGAGCAGACGCTCCAGGCTGCGGCC 709
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 676 TGGCGCGCTTCTTCAGAGAGGCCAAG---GGACTTGTCTTTTATTTCGGTGAGCTACCC 732
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 710 CATGGGACTTCTTTAAGAAACCAAGGGCGGCTGGATTCTACTTTCGGTGAATCGCCC 769
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 733 CTCTCTTTGGCGCTTGACCAAGCAGTGGATGTGTGAAGCTACCTCTCTGGAGAACCCA 792
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 770 CTGTCTCTGGCGGTGACCAACACAGCTGGGCACTGTGAAGTTCTTCTGCTGCAGAACTCC 829
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 793 CACCAGCCCGCAGCTGCGAGCCCACTGACTCCAGGGGCAACACAGACTCTGSCATGCCCTA 852
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 830 TGGCAGAGCGCGACATCAGCGCCAGGGACTCGGTGGGCAACACGCTGTCACGCGCTG 889
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 853 GTGATGATCTCGGACAACTAGCTGAGAACTATTGCACTGTGTGACAGCATGTATGATGGG 912
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 890 GTGGAGGTGGCGGCAACACAGCGCGCAACACAGAAATTTGTGACGAGCATGTACAATGAG 949
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 913 CTCCTCCAAGCTGGGGCGGCTCTGCCCTACCGTGCAGCTTGGAGCATCCGAACTCG 972
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 950 ATCTGATCTCTGAGGCGGCAAACTGACCCGAGCTGAAAGCTTGGAGAGCTCACCAACAG 1009
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 973 CAGGATCTCAGGCTCTGAAGCTGGCGCGCCAGGAGGGCAAGATCGAGATTTTCAGGCAC 1032
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1010 AAGGAATGACGCCCTGGCTCTGGCAGCTGGGACCTGGGAGAGCAACATCTGGAAAGCTG 1069
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Qy 1033 ATCTGTCAGCGGAGTT-----TTCAGGACTGAGCCACCTTTTCCGAAAGTTTACCAG 1086
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1070 ATTCTCCAGCGGAGATCCAGGAGCCGAGTCCAGGACCTGTCCAGGAAGTTTCCCGAG 1129
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1087 TGGTGTATGGGCTGTGTCGGGTGTGCTGTATGAGCTTGTCTGTGACAGCTGTGAG 1146
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1130 TGGGCTTACGGGCGCGTGCACTCTCGCTGTAGACCTTCTCCTGCACTGCAACCTCGGAG 1189
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1147 GAGAACTCAGTCTGAGAGATCATTTGCTTTTCAATTGCA---AGAGCCCGCACCCACACCGA 1203
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1190 AAGAACTCGGTCTGGAGGTGATCGCTACAGCAGCAGCGAGACCCCTTATCGCCAGCAG 1249
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1204 ATGGTCTGTTTGGAGCCCTGAAACAACTGCTGAGCGGCAAAATGGGA---TCTGTCTCATC 1260
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1250 ATGCTCTTGGTGGAGCGCTGAAACCGACTCTCTGACGACAAGTGGGACAGATTCGTCAAG 1309
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1261 CCCAAGTCTTCTTAAACTTCTGTGTATCTGATCTACATGTTCATCTTCACGGCTGTT 1320
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1310 CGCATCTTCTACTTCAACTTCTCTGGTCTACTGCTGTATCATGATCATCTTTCACCATGGCT 1369
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1321 GCTTACCATCAGCTTACCCTGAAAGCAGGCGCGCCCTCACCTGAAAGCGGAGTTGGA 1380
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1370 GCTTACTACAGGCC-----CGTGGATGGCTTGCCTCCCTTTAAGATGGAAAAAATGGA 1423
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1381 AACTCCATGCTGTGACGGGCCACATCTTATCTCTGTAGGGGGGATCTACCTCTCTGTTG 1440
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1424 GACTATTTCCGAGTTACTGGAGAGATCTCTGTGTGTAGGAGGAGTCTACTTCTTTTTC 1483
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1441 GGCACGCTGTGTACTTCTGCGGCGCCAGTGTTCATCTGGATCTCGTTTCATAGACAGC 1500
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1484 CGAGGATTCAGTATTTCTCTGACAGAGCGGCCGTCGATGAAGACCCCTGTTTGTGGACAGC 1543
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1501 TACTTTGAAATCTCTTCTCTGTTTCCAGGCCCTCTCACAGTGTGTCCACAGTGTCTGTGT 1560
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1544 TACAGTGAGATGCTTTTCTTCTGCACTACTGTTTATGCTGGCCACCGTGGTGTCTGTAC 1603
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1561 TTCTCTGGCCATCAGTGTGTACTCTGCTTGTGTGTCTGCGCTGTGTGTGGGTGTGGCTG 1620
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1604 TTACAGCCACTCAAGGAGTATGTGGCTTCCATGTATTTCTCTCTGGCTTGGGTGTGACC 1663
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1621 AACCTGTTTATATACGTGTGCTTCCAGACACAGGCACTTACAGTGTCTCATGATCCAG 1680
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1664 AACATGCTCTACTACACCCCGGCTTCCAGCAGATGGGCATCTATGCGCTCATGATAGAG 1723
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1681 AAGGTCACTCTGCGGACCTGCTGCGCTTCTTCTGATCTACTTTAGTCTTCTCTTTCGCG 1740
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1724 AAGATGATCTGAGAGACCTGTGCCGTTTCTATGTTGTCTACGTCTCTTCTTCTGTTGG 1783
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1741 TTGCTGTAGCCCTGTGTGAGCTTGAGCCAGGAGGCTTTGGCGCCCGCCGAAGCTCTTACAGGC 1800
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1784 TTTTCCACAGCGGTGGTGACGCTGATTGAAGACGGGAAGAAATGACTCCCTGCGCTCTGAG 1843
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1801 CCCAATGCCACAGATCAGTGTGAGCCCATGAGGGGACAGAGGACGAGGGGCAACGGGGCC 1860
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1844 TCCACGTC-----GCACAGGTGGCGGGGCTGCTGTCAGGCGCCCGCCGATAGC 1891
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1861 CAGTACAGGGGTATCTTGAAGGCTCTCTGAGAGCTTTCAAAATTCACCATCGGATGGGC 1920
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1892 TCCTTACAAAGCCTGTACTCCACTGCTGAGCTGTTCAAGTTTCAATCGGATGGGC 1951
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1921 GAGCTGGCTTCCAGGAGCAGCTGCACTTCCGCGGCAATGGTGTCTGTCTGTCTGTCTGCGC 1980
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1952 GACTGAGTTCACTGAGAACTATGACTTCAAGGCTGTCTTTCATCATCTCTGCTGTGCGC 2011
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1981 TACGTGTCTCTACCTACATCTCTGCTCAATGTCTCATGCGCCTCATGAGCAGAC 2040
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 2012 TATGTAATTTCTACCTACATCTCTCTGCTCAACATGTCTCATGCGCCTCATGGGTGAGACT 2071
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 2041 GTCAAGAGTGTCCCACTGACGTGGAGCATCTGGAAGCTGCAAGAAGCCATCTCTGTCT 2100
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 2072 GTCACAAAGATCGCACAGGAGCAAGAAACATCTGGAAAGCTGCGAGAGGCCATCACCATC 2131
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Qy	2101	CTGGAGATGGAGATGGCTATTGGTGTGTCAGGAAGAAG---CAGCGGGCAGGTGTGATG	2157
Db	2132	CTGGACACGGAGAAAGAGCTTCCTTAAGTGCATGAGGAAGGCCCTTCGCTCAGGCAAGCTG	2191
Qy	2158	CTGACCGTTGGCACTAAGCCAGATGCCGCCGATGAGCGCTGTGCTTCAGGGTGGAG	2217
Db	2192	CTGCAGGTGGGTACACACCTGATGGCNAGGACGACTACCGGTGGTGTCTCAGGGTGGAC	2251
Qy	2218	GAGGTGAACCTGGGCTTTCATGGGAGCAGACGCTGCCTACGCTGTGTGAGGACCCG	2271
Db	2252	GAGGTGAACCTGGACCACTGGAACACCAACGTTGGGCATCATCAACGAAGACCCG	2305

Search completed: October 6, 2005, 22:59:28  
Job time : 441 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 17:19:16 ; Search time 7208 Seconds  
(without alignments)  
13038.385 Million cell updates/sec

Title: US-09-445-614B-1  
Perfect score: 2469  
Sequence: 1 cagcaggcgcagcagct.....gctggtctggggctccagct 2469

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- EST.\*
- 1: gb\_est1.\*
  - 2: gb\_est2.\*
  - 3: gb\_est3.\*
  - 4: gb\_est4.\*
  - 5: gb\_est5.\*
  - 6: gb\_est6.\*
  - 7: gb\_est7.\*
  - 8: gb\_est8.\*
  - 9: gb\_est9.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1581.2	64.0	2760	3 AK089004	AK089004 Mus muscu
2	1505.8	61.0	2270	3 AK008689	AK008689 Mus muscu
3	884.6	35.8	962	5 BQ652688	BQ652688 AGENCOURT
4	871.6	35.3	933	5 BQ678083	BQ678083 AGENCOURT
5	866	35.1	940	5 BQ645005	BQ645005 AGENCOURT
6	851.2	34.5	902	5 BQ650623	BQ650623 AGENCOURT
7	850	34.4	907	5 BQ653925	BQ653925 AGENCOURT
8	849.2	34.4	945	5 BQ643665	BQ643665 AGENCOURT
9	829.2	33.6	871	5 BQ644508	BQ644508 AGENCOURT
10	819.8	33.2	1009	5 BQ064773	BQ064773 AGENCOURT
11	809.6	32.8	870	4 BG743115	BG743115 602634253
12	804.6	32.6	862	5 BQ643779	BQ643779 AGENCOURT
13	785.2	32.2	3674	3 AK038307	AK038307 Mus muscu
14	793.6	32.1	915	5 BQ638756	BQ638756 AGENCOURT
15	786	31.8	941	5 BQ653113	BQ653113 AGENCOURT
16	778	31.5	922	5 BQ643949	BQ643949 AGENCOURT
17	775	31.4	957	5 BQ644054	BQ644054 AGENCOURT
18	772.2	31.3	880	4 BG764899	BG764899 602737335
19	754.2	30.5	785	4 BG765155	BG765155 602737587
20	744.8	30.2	951	4 B1819175	B1819175 603036979
21	705.2	28.6	886	5 BQ644271	BQ644271 AGENCOURT
22	693.4	28.1	976	5 BQ679954	BQ679954 AGENCOURT
23	691.8	28.0	753	6 CD365397	CD365397 UI-H-FT2-
24	690.4	28.0	751	6 CA432218	CA432218 UI-H-FG1-

25	688.6	27.9	793	1 AU141855	AU141855 AU141855
26	685.8	27.8	926	6 CD513620	CD513620 AGENCOURT
c 27	676.6	27.4	757	5 BU617949	BU617949 UI-H-DF0-
28	675.8	27.4	756	4 BM007978	BM007978 603617714
c 29	670.6	27.2	742	6 CB528322	CB528322 UI-H-FT2-
30	662.6	26.8	753	5 BX339344	BX339344 BX339344
31	662.4	26.8	4187	3 HSM801769	ALI136801 Homo sapi
c 32	662	26.8	711	7 CN480858	CN480858 UI-H-FT2-
33	660.6	26.8	712	6 CD627522	CD627522 55109895H
34	651.4	26.4	953	4 BG254423	BG254423 602369021
c 35	644.4	26.1	901	5 BU190985	BU190985 AGENCOURT
c 36	630.2	25.5	686	2 AW976725	AW976725 EST388834
37	629.8	25.5	896	5 BU540815	BU540815 AGENCOURT
38	625	25.3	625	7 CV027855	CV027855 6217 Full
39	622.4	25.2	970	5 BQ888238	BQ888238 AGENCOURT
c 40	596.2	24.1	682	2 BF732920	BF732920 nael7b01.
41	588	23.8	588	2 BF940288	BF940288 7043f06.x
c 42	585	23.7	585	5 BP304605	BP304605 BP304605
43	580.2	23.5	872	4 BG765286	BG765286 602738720
c 44	578.4	23.4	616	1 AI801897	AI801897 tx28h02.x
c 45	577.4	23.4	632	5 BU632884	BU632884 UI-H-FE1-

## ALIGNMENTS

RESULT 1	AK089004	2760 bp	mrna	linear	HTC 03-APR-2004
LOCUS	Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430035F12 product:vanilloid receptor-like protein 1, full insert sequence.				
DEFINITION	AK089004.1 GI:26354129				
ACCESSION	AK089004				
VERSION	HTC; CAP trapper.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalisation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
REFERENCE	5				
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research				



Db 1319 AGCGGAGTTCTCAGGGCTGTACACAGCCCTTTCCGAAAGTTTACCGAGTGTGTCTACG 1378  
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Qy 2411 -GGCAGAGCAGCAGCAGCAGGATCTTTCCACCATCTGCTGGCTCTG 2459  
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## RESULT 2

AK008689 2270 bp mRNA linear HTC 03-APR-2004  
LOCUS Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210009M20 product:vanilloid receptor-like protein 1, full insert sequence.  
DEFINITION  
ACCESSION AK008689.1 GI:12843037  
VERSION HTC; CAP trapper.  
KEYWORDS Mus musculus (house mouse)  
SOURCE  
ORGANISM  
REFERENCE  
1 Carninci, P. and Hayashizaki, Y.  
AUTHORS High-efficiency full-length cDNA cloning  
TITLE Meth. Enzymol. 303, 19-44 (1999)  
JOURNAL 99279253  
MEDLINE 10349636  
PUBMED  
REFERENCE  
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
AUTHORS Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
TITLE Genome Res. 10 (10), 1617-1630 (2000)  
JOURNAL 20499374  
MEDLINE 11042159  
PUBMED  
REFERENCE  
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsuoka, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
AUTHORS RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
TITLE Genome Res. 10 (11), 1757-1771 (2000)  
JOURNAL 20530913  
MEDLINE 11076861  
PUBMED  
REFERENCE  
4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.  
AUTHORS Functional annotation of a full-length mouse cDNA collection  
TITLE Nature 409, 685-690 (2001)  
JOURNAL  
REFERENCE  
5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
AUTHORS Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
TITLE Nature 420, 563-573 (2002)  
JOURNAL













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ACCESSION	BQ649665		
VERSION	BQ649665.1 GI:21773837		
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ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 945)		
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a>		

Tissue Procurement: CGAP (Stanford) cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LICM2514 row: g column: 09 High quality sequence stop: 572. Location/Qualifiers 1. .945 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6300320" /tissue type="hepatocellular carcinoma, cell line" /lab host="DH10B (phage-resistant)" /clone lib="NIH_MGC_100" /note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."									
FEATURES									
source	Query Match	34.4%	Score 849.2;	DB 5;	Length 945;				
	Best Local Similarity	96.5%;	Pred. No. 9e-194;						
	Matches 888;	Conservative 0;	Mismatches 27;	Indels 5;	Gaps 2;				
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DB	121	CTGTGTCTGGGTGCTGCTGAACTGCTTTACTATATACCGTGGCTTCCAGCACACAGGCATC	180						
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Tissue Procurement: CGAP (Stanford)  
cDNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at:  
<http://image.llnl.gov>  
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FEATURES		source
ORIGIN		
Query Match		34.4%; Score 849.2; DB 5; Length 945;
Best Local Similarity		96.5%; Pred. No. 9e-194;
Matches		888; Conservative 0; Mismatches 27; Indels 5; Gaps 2;
Qy	1483	ATCTCGTTTCATAGACAGCTACTTTGAAATCCTTCTTCCAGCCATCGAGTGTACCTGCCCCTGCTGTGTCTGCG 1542
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Qy	1723	TTAGTCTTCTTTCGCTTTCGCTGTAGCCCTGCTGAGCCCTGAGCCAGGAGCTTGGCGC 1782
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Qy	1843	GACAGGGCAACGGGGCCAGTACAGGGGTATCTTGAAGCTCTTCTTGGAGCTCTTCAA 1902
Db	361	GACAGGGCAACGGGGCCAGTACAGGGGTATCTTGAAGCTCTTCTTGGAGCTCTTCAA 420
Qy	1903	TTCAACCATCGGCATGGGCGAGCTGGCTTCCAGGAGCAGCTGCACTTCCGCGGATGGT 1962
Db	421	TTCAACCATCGGCATGGGCGAGCTGGCTTCCAGGAGCAGCTGCACTTCCGCGGATGGT 480
Qy	1963	CTGCTGTCTGTGGCTTACGTGTCTGCTCACTATCTGCTGTCTCAACATGCTCATC 2022
Db	481	CTGCTGTCTGTGGCTTACGTGTCTGCTCACTATCTGCTGTCTCAACATGCTCATC 540
Qy	2023	GCCTCATGAGCGAGCCGTCACAGTGTGCGCCATGACAGCTGGAGCATCTGGAAGCTG 2082
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: gcapbs-femail.nih.gov
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Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2489 row: n column: 14
High quality sequence stop: 672.
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
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ORIGIN

Query Match 33.6%; Score 829.2; DB 5; Length 871;

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Db 617 TCGAAGAACCCATCTCTGCTGGAGATGGAGATGGCTATTGGTGGTCAGAGAGAGC 676
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QY 2141 AGCGGCGAGTGTGTGTGCTGTGACCGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCT 2200
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Db 677 AGCGGCGAGTGTGTGTGCTGTGACCGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCT 736
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QY 2201 GGTGTCTTCAGGGTGGAGGAGTGAACTGGGCTTTCATGGGAGCAGAGCTGCGCTTACGCTGT 2260
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Db 737 GGTGTCTTCAGGGTGGAGGAGTGAACTGGGCTTTCATGGGAGCAGAGCTGCGCTTACGCTGT 796
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QY 2261 GTGAGGACCCGTGAGGGGAGAGTGTCCCTCGAATCTTCAGAACCCCTGTCTTCTTCC 2319
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Db 797 GTGAGGACCCGTGAGGGGAGAGTGTCCCTCGAATCTTCAGAACCCCTGTCTTCTTCC 856
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QY 2320 CTCTCCCAAGGAGGA 2333
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Db 857 CTCTCCCAAGGAGGA 870
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RESULT 10

BQ064773

LOCUS

DEFINITION

AGENCOURT\_6853681 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5926530

5', mRNA sequence.

ACCESSION

BQ064773

VERSION

BQ064773.1

GI:19893722

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

BQ064773 BQ064773 1009 bp mRNA linear EST 02-APR-2002

AGENCOURT\_6853681 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5926530

5', mRNA sequence.

ACCESSION BQ064773

VERSION BQ064773.1

GI:19893722

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1009)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: Lou Staudt cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLCM2099 row: p column: 19 High quality sequence stop: 628. Location/Qualifiers
FEATURES	1..1009 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5926530" /tissue_type="lymphoma, cell line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 99" /notes="Organ: Lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN	Query Match 33.2%; Score 819.8; DB 5; Length 1009; Best Local Similarity 98.0%; Pred. No. 1.2e-186; Matches 872; Conservative 0; Mismatches 13; Indels 5; Gaps 4;  QY 1483 ATCTCGTTTCATACAGAGCTACTTTGAAATCTCTTCCTGTTCCAGGCCCTGCTCACAGTG 1542 DB 1 ATCTCGTTTCATACAGAGCTACTTTGAAATCTCTTCCTGTTCCAGGCCCTGCTCACAGTG 60  QY 1543 GTGTCCAGGTGCTGTGTTTCTGGCCATCGAGTGTACCTGCCCTGCTGTCTGCTGCG 1602 DB 61 GTGTCCAGGTGCTGTGTTTCTGGCCATCGAGTGTACCTGCCCTGCTGTGCTGCG 120  QY 1603 CTGTGCTGGGCTGGCTGAACCTGCTTTACTATACACGTGGCTTCCAGCACACAGGCATC 1662 DB 121 CTGTGCTGGGCTGGCTGAACCTGCTTTACTATACAGTGGCTTCCAGCACACAGGCATC 180  QY 1663 TACAGTGTCTATGATCCAGAGAGTTCATCTCGCGGACCTGCTCGCTTCTTCTGATCTAC 1722 DB 181 TACAGTGTCTATGATCCAGAGAGTTCATCTCGCGGACCTGCTCGCTTCTTCTGATCTAC 240  QY 1723 TTAGTCTTCTTTTCGGCTTCGCTGTAGCCCTGGTGGAGCTGAGCCAGGAGCTTGGCGC 1782 DB 241 TTAGTCTTCTTTTCGGCTTCGCTGTAGCCCTGGTGGAGCTGAGCCAGGAGCTTGGCGC 300  QY 1783 CCCGAAGCTCTTACAGSCCCCAATGCCACAGAGTCACTGACGCCATGGAGGACAGGAG 1842 DB 301 CCCGAAGCTCTTACAGSCCCCAATGCCACAGTCACTGACGCCATGGAGGACAGGAG 360  QY 1843 GACGAGGGCAACCGGGGCCAGTACAGGGGTATCCTTGGAAAGCTTCTTGGAGCTTCTTCAA 1902 DB 361 GACGAGGGCAACCGGGGCCAGTACAGGGGTATCCTTGGAAAGCTTCTTGGAGCTTCTTCAA 420  QY 1903 TTCAACATCGGCATGGCGAGCTGGCTTCCAGGACAGCTGCACCTTCGGCGCATGTG 1962 DB 421 TTCAACATCGGCATGGCGAGCTGGCTTCCAGGACAGCTGCACCTTCGGCGCATGTG 480

Matches	840;	Conservative	0;	Mismatches	14;	Indels	2;	Gaps	2;
QY	1490	TCATAGACAGCTACTTTGAAATCCTTCTCTGTTTCAGGCGCTGCTCAGAGTGGTGTCCC	1549						
Db	2	TCATAGACAGCTACTTTGAAATCCTTCTCTGTTTCAGGCGCTGCTCAGAGTGGTGTCCC	61						
QY	1550	AGGTGCTGTGTTTCTCGGCATCAGTGGTACCTGCGCCCTGCTGTGCTGCGCTGTGC	1609						
Db	62	AGGTGCTGTGTTTCTCGGCATCAGTGGTACCTGCGCCCTGCTGTGCTGCGCTGTGC	121						
QY	1610	TGGGCTGGCTGAACCTGCTTTTACTATACAGTGGCTTTCAGACACAGGCGATCTACAGTG	1669						
Db	122	TGGGCTGGCTGAACCTGCTTTTACTATACAGTGGCTTTCAGACACAGGCGATCTACAGTG	181						
QY	1670	TCATGATCCAGAAAGGTGATCCTCGGGAAGCTGCTGCGCTTCTTCTGATCTATTAGTCT	1729						
Db	182	TCATGATCCAGAAAGGTGATCCTCGGGAAGCTGCTGCGCTTCTTCTGATCTATTAGTCT	241						
QY	1730	TCCTTTTTCGGCTTCGCTGTAGCCCTGGTGAGCTGAGCGAGGCTTGGCGCCCGAAG	1789						
Db	242	TCCTTTTTCGGCTTCGCTGTAGCCCTGGTGAGCTGAGCGAGGCTTGGCGCCCGAAG	301						
QY	1790	CTCTACAGGCCCCCAATGCCACAGAGTCAGTGCAGGCCCATGGAGGACAGGAGCGAGG	1849						
Db	302	CTCTACAGGCCCCCAATGCCACAGAGTCAGTGCAGGCCCATGGAGGACAGGAGCGAGG	361						
QY	1850	GCAACGGGGCCAGTACAGGGGTATCTGGAAGCTTCTTGGAGCTTCTTCAAAATTACCA	1909						
Db	362	GCAACGGGGCCAGTACAGGGGTATCTGGAAGCTTCTTGGAGCTTCTTCAAAATTACCA	421						
QY	1910	TCCGCTAGGCGAGCTGGCTTCCAGGAGCAGCTGCATCTCCGCGCATGCTGCTGCTC	1969						
Db	422	TCCGCTAGGCGAGCTGGCTTCCAGGAGCAGCTGCATCTCCGCGCATGCTGCTGCTC	481						
QY	1970	TGCTGTGGCTACGTGCTGCTCACTTACATCTGCTGCTCAACATGCTCATCGCCCTCA	2029						
Db	482	TGCTGTGGCTACGTGCTGCTCACTTACATCTGCTGCTCAACATGCTCATCGCCCTCA	541						
QY	2030	TGAGCGAGACCGTCAACAGTGTGCCACTGACAGCTGGAGCATCTGGAAGCTGCAGAAAG	2089						
Db	542	TGAGCGAGACCGTCAACAGTGTGCCACTGACAGCTGGAGCATCTGGAAGCTGCAGAAAG	601						
QY	2090	CCATCTCTGCTGGAGATGGAAATGGCTATTTGGTGGTGCAGGAGACGCGGCGAG	2149						
Db	602	CCATCTCTGCTGGAGATGGAAATGGCTATTTGGTGGTGCAGGAGACGCGGCGAG	661						
QY	2150	GTGTGATGCTGACCG-TTGGCACTAAGCCAGATGGCAGCGCCGATGAGCGCTGGTCTTC	2208						
Db	662	GTGTGATGCTGACCGTTTGGCACTAAGCCAGATGGCAGCGCCGATGAGCGCTGGTCTTC	721						
QY	2209	AGGCTGAGAGGTGAACCTGGCTTTCATGGAGACAGCGTGGCTTA-CGCTGTGTGAGGA	2267						
Db	722	AGGCTGAGAGGTGAACCTGGCTTTCATGGAGACAGCGTGGCTTA-CGCTGTGTGAGGA	781						
QY	2268	CCGCTCAGGGGAGGTGCTCCTCGAATCTTCGAGAACCTGCTGCTGCTCCCTCCCA	2327						
Db	782	CCGCTCAGGGGAGGTGCTCCTCGAATCTTCGAGAACCTGCTGCTGCTCCCTCCCA	841						
QY	2328	GGAGGATGAGGATGGT 2343							
Db	842	GGATGAGATGGTGTCT 857							

RESULT 12  
 BU838779  
 LOCUS  
 DEFINITION BU838779 862 bp mRNA linear EST 16-OCT-2002  
 AGENCOURT\_8210115 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6258039  
 5', mRNA sequence.  
 ACCESSION BU838779  
 VERSION BU838779.1 GI:24023174  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 862)
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2413 row: e column: 16 High quality sequence stop: 653.
FEATURES	Location/Qualifiers
Source	1..862 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6258039" /tissue_type="melanotic melanoma, cell line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 112" note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN	Query Match 32.6%; Score 804.6; DB 5; Length 862; Best Local Similarity 98.9%; Pred. No. 5.2e-183; Matches 842; Conservative 0; Mismatches 4; Indels 5; Gaps 3;
QY	1191 GCACCGACACCGAATGGTGGTGGAGCCCTCGAACAACTGCTGCGAGCGAAATGGGA 1250
Db	1 GCACCGACACCGAATGGTGGTGGAGCCCTCGAAC-AACTGCTGCGAGCGAAATGGGA 59
QY	1251 TCTGTCTATCCCCAAGTCTTCTTAAACTTCTGTGTATCTGATCTATCTTCTTCTT 1310
Db	60 TCTGTCTATCCCCAAGTCTTCTTAAACTTCTGTGTATCTGATCTATCTTCTTCTT 119
QY	1311 CACCGCTGTGCTTACATCAGCTACCTGAGAGAGCAGCGCCGCTCACCTGAAAGC 1370
Db	120 CACCGCTGTGCTTACATCAGCTACCTGAGAGAGCAGCGCCGCTCACCTGAAAGC 176
QY	1371 GGAGGTGGAAACTCCATGCTGTCAGCGGCCACATCCCTTATCTCTGTAGGGGGATCTA 1430
Db	177 GGAGGTGGAAACTCCATGCTGTCAGCGGCCACATCCCTTATCTCTGTAGGGGGATCTA 236
QY	1431 CCTCTCTGTGGCCAGCTGTGTACTTCTGCGGGCCACGCTGTCATCTGGATCTCGTT 1490
Db	237 CCTCTCTGTGGCCAGCTGTGTACTTCTGCGGGCCACGCTGTCATCTGGATCTCGTT 296
QY	1491 CATAGACAGCTACTTTTGAATCTCTTCTGTTTCCAGGCGCTGCTCACAGTGTGTCCCA 1550
Db	297 CATAGACAGCTACTTTTGAATCTCTTCTGTTTCCAGGCGCTGCTCACAGTGTGTCCCA 356
QY	1551 GGTGTGTGTCTTCTGGCCATCGAGTGGTACTTGGCCCTGCTGTGTGTGTGTGTGTGTGT 1610
Db	357 GGTGTGTGTCTTCTGGCCATCGAGTGGTACTTGGCCCTGCTGTGTGTGTGTGTGTGTGT 416
QY	1611 GGGCTGGCTGAACCTGCTTTTATATACAGTGGCTTCCAGCACACAGGATCTTACAGTGT 1670
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QY	1671 CATGATCCAGAAAGGTTCATCTCGGGAGCCTGCTGCGCTTCTTCTTCTTCTTCTTCTT 1730

Db	477	CATGATCCAGAGGTATCTCTGGGACCTGCTGGCTTCTCTGATCTACTACTGCTT	536
Qy	1731	CTTTTCGGGTTTCGCTGTAGCCCTGTGAGCCCTGAGCAGGAGGCTTGGGGCCCCGAAGC	1790
Db	537	CTTTTCGGGTTTCGCTGTAGCCCTGTGAGCCCTGAGCAGGAGGCTTGGGGCCCCGAAGC	596
Qy	1791	TCCTACAGGCCCCCAATGCCACAGATCAGTGCAGGCCCATGAGGGACAGGAGGACGAGG	1850
Db	597	TCCTACAGGCCCCCAATGCCACAGATCAGTGCAGGCCCATGAGGGACAGGAGGACGAGG	656
Qy	1851	CAACGGGGCCCACTACAGGGGTTCTCTGGAAGCTCTCTTGGAGCTCTTCAAAATTCACCAT	1910
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Qy	1911	CGGATGCGGCGAGCTGCGCTTCCAGGAGCAGTGCACCTCCGGGGCATGCTGCTGCTGCT	1970
Db	717	CGGATGCGGCGAGCTGCGCTTCCAGGAGCAGTGCACCTCCGGGGCATGCTGCTGCTGCT	776
Qy	1971	GCTGCTGGCTTACGTGCTGCTCACCTACATCTGCTGCTCAACATGCTCATC-GCCTCA	2029
Db	777	GCTGCTGGCTTACGTGCTGCTCACCAACATCTGCTGCTCAACATGCTCATC-GCCTCA	836
Qy	2030	TGAGCCGAGACC	2040
Db	837	TGAGCCGAGAAC	847
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LOCUS		Mus musculus 16 days neonate thymus cDNA, RIKEN full-length	
DEFINITION		enriched library, clone:AI30094L01 product:vanilloid receptor-like	
ACCESSION		protein 1, full insert sequence.	
VERSION		AK038307.1 GI:26086445	
KEYWORDS		HTC; CAP trapper.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE		Carninci, P. and Hayashizaki, Y.	
JOURNAL		High-efficiency full-length cDNA cloning	
MEDLINE		Meth. Enzymol. 303, 19-44 (1999)	
PUBMED		99279253	
REFERENCE		2 10349636	
AUTHORS		Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,	
TITLE		Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
JOURNAL		Normalization and subtraction of cap-trapper-selected cDNAs to	
MEDLINE		prepare full-length cDNA libraries for rapid discovery of new genes	
PUBMED		Genome Res. 10 (10), 1617-1630 (2000)	
REFERENCE		20499374	
AUTHORS		11042159	
TITLE		Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,	
JOURNAL		Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,	
MEDLINE		Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,	
PUBMED		Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,	
REFERENCE		Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,	
AUTHORS		Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,	
TITLE		Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
JOURNAL		RIKEN integrated sequence analysis (RISA) system--384-format	
MEDLINE		sequencing pipeline with 384 multicapillary sequencer	
PUBMED		Genome Res. 10 (11), 1757-1771 (2000)	
REFERENCE		20530913	
AUTHORS		11076861	
TITLE		The RIKEN Genome Exploration Research Group Phase II Team and the	
JOURNAL		FANTOM Consortium.	
MEDLINE		Functional annotation of a full-length mouse cDNA collection	
PUBMED		Nature 409, 685-690 (2001)	
REFERENCE		4	
AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the	
TITLE		FANTOM Consortium.	
JOURNAL		Functional annotation of a full-length mouse cDNA collection	
MEDLINE		Nature 409, 685-690 (2001)	
PUBMED		11076861	
REFERENCE		4	
AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the	
TITLE		FANTOM Consortium.	
JOURNAL		Functional annotation of a full-length mouse cDNA collection	
MEDLINE		Nature 409, 685-690 (2001)	
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JOURNAL		Functional annotation of a full-length mouse cDNA collection	
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AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the	
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MEDLINE		Nature 409, 685-690 (2001)	
PUBMED		11076861	
REFERENCE		4	
AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the	
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JOURNAL		Functional annotation of a full-length mouse cDNA collection	
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PUBMED		11076861	
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AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the	
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MEDLINE		Nature 409, 685-690 (2001)	
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MEDLINE		Nature 409, 685-690 (2001)	
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JOURNAL		Functional annotation of a full-length mouse cDNA collection	
MEDLINE		Nature 409, 685-690 (2001)	
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AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the	
TITLE		FANTOM Consortium.	
JOURNAL		Functional annotation of a full-length mouse cDNA collection	
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AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the	
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AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the	
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JOURNAL		Functional annotation of a full-length mouse cDNA collection	
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JOURNAL		Functional annotation of a full-length mouse cDNA collection	
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JOURNAL		Functional annotation of a full-length mouse cDNA collection	
MEDLINE		Nature 409, 685-690 (2001)	
PUBMED		11076861	
REFERENCE		4	
AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the	
TITLE		FANTOM Consortium.	
JOURNAL		Functional annotation of a full-length mouse cDNA collection	
MEDLINE		Nature 409, 685-690 (2001)	
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MEDLINE		Nature 409, 685-690 (2001)	
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AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the	
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TITLE		FANTOM Consortium.	
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TITLE		FANTOM Consortium.	
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TITLE		FANTOM Consortium.	
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MEDLINE		Nature 409, 685-690 (2001)	
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TITLE		FANTOM Consortium.	
JOURNAL		Functional annotation of a full-length mouse cDNA collection	
MEDLINE		Nature 409, 685-690 (2001)	
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TITLE		FANTOM Consortium.	
JOURNAL		Functional annotation of a full-length mouse cDNA collection	
MEDLINE		Nature 409, 685-690 (2001)	
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VERSION BU838756.1 GI:24023151  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
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NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTF  
cDNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILLNL at:  
http://image.llnl.gov  
Plate: LLCM2413 row: d column: 16  
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into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

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AUTHORS				
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JOURNAL				
COMMENT				
NIH-MGC http://mgc.nci.nih.gov/.				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				
Email: cgapbs-remail.nih.gov				
Tissue Procurement: CGAP (Stanford)				
cDNA Library Preparation: Rubin Laboratory				
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
DNA Sequencing by: Agencourt Bioscience Corporation				
Clone distribution: MGC clone distribution information can be				
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GGCAGAG(G). Size-selected >500bp for average insert size				
1.8kb. Library constructed by Ling Hong in the laboratory				
of Gerald M. Rubin (University of California, Berkeley)				
using ZAP-cDNA synthesis kit (Stratagene) and Superscript				
II RT (Life Technologies). Note: this is a NIH_MGC				
Library."				
FEATURES				
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Matches 869; Conservative 0; Mismatches 39; Indels 12; Gaps 5;				
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Job time : 7219 secs				

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 14:22:24 ; Search time 1224 Seconds  
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11941.047 Million cell updates/sec

Title: US-09-445-614B-1

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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	2462.2	99.7	2809	13 Adq89073	Adq89073 Human uro
5	2460.6	99.7	2774	13 Adq83962	Adq83962 Human tum
6	2460.6	99.7	2807	13 ADP25060	Adp25060 PRO polyt
7	2455.8	99.5	2825	4 Aaa09554	Aaa09554 Human tra
8	2447.4	99.1	2867	6 ABL90839	Ab190839 Human pol
9	2444.6	99.0	2783	2 AAZ22829	Aaz22829 Human van
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12	2424.6	98.2	2805	9 ACD91294	Ac91294 Human van
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15	2347.8	95.1	2351	2 AAZ07114	Aaz07114 Human van
16	2333.4	94.5	2348	2 AAZ07116	Aaz07116 Human van
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43	750.8	30.4	884	2 AAX19741	Aax19741 Human VRR
44	750.4	30.4	885	2 AAZ07115	Aaz07115 Human van
45	711	28.8	876	2 AAV59808	Aav59808 Human sec

## ALIGNMENTS

### RESULT 1

AAC60297

ID AAC60297 standard; DNA; 2469 BP.

XX

AC AAC60297;

DT 14-FEB-2001 (first entry)

XX Human vanilloid receptor like receptor DNA.

XX VR-L; vanilloid receptor-like receptor; pain; infection; allergy;  
mechanical injury; lymphoid tissue; human; ds.

XX Homo sapiens.

PN GB2346882-A.

XX 23-AUG-2000.

XX 02-DEC-1999; 99GB-00028566.

XX 08-DEC-1998; 98GB-00027016.

XX (MERI ) MERCK SHARP & DOHME LTD.

XX Bonbert TP;

XX WPI; 2001-064250/08.

DR P-PSDB; AAB35622.

XX New polynucleotide encoding human vanilloid receptor-like receptor for  
diagnosing and treating pain, infections, allergies, and cancers.

PS Claim 2; Fig 1; 36pp; English.

XX The present invention relates to the human vanilloid receptor-like  
receptor. This receptor may be used for diagnosing or treating conditions  
associated with altered vanilloid receptor-like (VR-L) receptor  
expression. It may also be used to treat abnormal conditions associated  
with pain. Conditions or diseases that can be diagnosed or treated  
include viral, bacterial and fungal infections, allergic responses,  
mechanical injury associated with trauma, hereditary diseases, lymphoma  
or carcinoma, or other conditions which activate the genes of the



2041 GTCAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTC 2100  
2101 CTGGAGATGAGATGGCTATTGGTGTGTCAGGAGAGACAGCGGCGAGGTGTGATGCTG 2160  
2101 CTGGAGATGAGATGGCTATTGGTGTGTCAGGAGAGACAGCGGCGAGGTGTGATGCTG 2160  
2161 ACCGTTGGCACTAAGCCAGATGCGACCGCGATGAGCGTGTGCTTCAAGGTTGGAGGAG 2220  
2161 ACCGTTGGCACTAAGCCAGATGCGACCGCGATGAGCGTGTGCTTCAAGGTTGGAGGAG 2220  
2221 GTGAATCGGCTTTCATGGAGCAGACGCTGCTTCAAGGTTGGAGGAG 2280  
2221 GTGAATCGGCTTTCATGGAGCAGACGCTGCTTCAAGGTTGGAGGAG 2280  
2281 GGTGTCCTTCGAACTTCGAGAACCTTCCTGGCTTCCCTCCCAAGGAGGATGAGGAT 2340  
2281 GGTGTCCTTCGAACTTCGAGAACCTTCCTGGCTTCCCTCCCAAGGAGGATGAGGAT 2340  
2341 GGTGTCCTTCGAGAAACTATGTGCCCGTCCAGCTCCTCCAGTCCCACTGATGGCCGAGA 2400  
2341 GGTGTCCTTCGAGAAACTATGTGCCCGTCCAGCTCCTCCAGTCCCACTGATGGCCGAGA 2400  
2401 TGCAGCAGAGGCGCAGAGCAGACAGCAGAGGATCTTTTCAACACATCTGCTGCTCTGG 2460  
2401 TGCAGCAGAGGCGCAGAGCAGACAGCAGAGGATCTTTTCAACACATCTGCTGCTCTGG 2460  
2461 GGTGCCAGT 2469  
2461 GGTGCCAGT 2469

RESULT 2

ADP66662  
ID ADP66662 standard; DNA; 2469 BP.  
XX  
AC ADP66662;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE Human vanilloid 2 receptor (VR2) polypeptide encoding DNA, SEQ ID 1.  
XX  
KW VR2; vanilloid 2 receptor; tranquilizer; antidepressant; hypnotic; CNS;  
KW tocolytic; vasotropic; hypotensive; cardiovascular; gynaecological;  
KW analgesic; neuroleptic; anticoagulant; gene therapy; human; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 97..2391  
FT /\*tag= a  
FT /product= "VR2 polypeptide"  
XX  
WO2004045638-A1.  
XX  
PD 03-JUN-2004.  
XX  
PF 18-NOV-2003; 2003WO-GB004988.  
XX  
PR 18-NOV-2002; 2002GB-00026850.  
PR 18-NOV-2002; 2002GB-00026865.  
PR 01-OCT-2003; 2003GB-00022990.  
XX  
PA (MERI ) MERCK SHARP & DOHME LTD.  
XX  
PI Oliver KR, Seabrook GR, Wainwright A;  
XX  
DR WPI; 2004-431843/40.  
DR P-PSDB; ADP66663.  
XX  
PT Use of vanilloid receptor-2 ligands for treating and/or preventing  
PT anxiety, depression, circadian rhythm disorders, pre-term labor, erectile  
PT dysfunction, hypertension, eclampsia and/or schizophrenia.

PS Claim 22; Fig 1; 46pp; English.  
XX  
The invention relates to a compound selected from a vanilloid 2 receptor  
(VR2) polypeptide, a compound which modulates the activity of a VR2  
polypeptide, a polynucleotide encoding a VR2 polypeptide, or an antisense  
polynucleotide. The compound is used for the manufacture of a medicament  
for treating anxiety, depression, circadian rhythm disorders, pre-term  
labour, erectile dysfunction, hypertension and/or schizophrenia. The compound may also be used  
for inducing diuresis and/or inhibiting platelet agglutination. The  
compound may also be used for manufacturing a medicament for treating the  
disorders mentioned above. The medicament enhances or improves sleep  
quality and/or is used for preventing and/or treating sleep disorders and  
sleep disturbances by increasing sleep efficiency and augmenting sleep  
maintenance in a mammal, or for achieving a circadian rhythm phase-  
shifting effect, for resetting the internal circadian clock or for  
shortening the time of reentrainment of circadian rhythms in a mammal.  
The present sequence represents a DNA encoding a human VR2 polypeptide.  
XX  
Sequence 2469 BP; 510 A; 724 C; 710 G; 525 T; 0 U; 0 Other;  
Query Match 100.0%; Score 2469; DB 12; Length 2469;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACGAGGCGCAGCGCAGCTGGGAGGAGACAGAGACCCCTTGACATCTCCATCTGCACAGA 60  
DB 1 CACGAGGCGCAGCGCAGCTGGGAGGAGACAGAGACCCCTTGACATCTCCATCTGCACAGA 60  
QY 61 GGTCTGTGTCGACCGCAGCAGCTCTCTCTCTAGATGACCTCACCTCCAGCTCTCCA 120  
DB 61 GGTCTGTGTCGACCGCAGCAGCTCTCTCTCTAGATGACCTCACCTCCAGCTCTCCA 120  
QY 121 GTTTTCAGGTTGGAGACATTAGATGAGGCCAAGAGATGGCTCTGAGCGGACAGAGGA 180  
DB 121 GTTTTCAGGTTGGAGACATTAGATGAGGCCAAGAGATGGCTCTGAGCGGACAGAGGA 180  
QY 181 AAGCTGGATTTTGGGAGCGGGCTGCCCTCCATGGAGTCAAGTTCCAGGCGGAGGACCGG 240  
DB 181 AAGCTGGATTTTGGGAGCGGGCTGCCCTCCATGGAGTCAAGTTCCAGGCGGAGGACCGG 240  
QY 241 AAATTCGCCCTCAGATAAGAGTCAACCTCACTACGAAAGGAAACAGTGCAGTCAG 300  
DB 241 AAATTCGCCCTCAGATAAGAGTCAACCTCACTACGAAAGGAAACAGTGCAGTCAG 300  
QY 301 CCGGATCCAAACCGATTTCACCGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTGTC 360  
DB 301 CCGGATCCAAACCGATTTCACCGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTGTC 360  
QY 361 GAGGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACAGCAAGTACCTCACCGACTCG 420  
DB 361 GAGGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACAGCAAGTACCTCACCGACTCG 420  
QY 421 GAATACACAGAGGGTCCACAGTAAGAGCTGCTGATGAGAGCTGTGCTGAACCTTAAG 480  
DB 421 GAATACACAGAGGGTCCACAGTAAGAGCTGCTGATGAGAGCTGTGCTGAACCTTAAG 480  
QY 481 GACGGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
DB 481 GACGGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
QY 541 CAGCCCTCTGTTAAATGCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCAC 600  
DB 541 CAGCCCTCTGTTAAATGCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCAC 600  
QY 601 ATCCGATTCAGAGAGGAGTCTGCGAGTGTGTAAGCTCTGCTGAGAGATGGGGCCAAT 660  
DB 601 ATCCGATTCAGAGAGGAGTCTGCGAGTGTGTAAGCTCTGCTGAGAGATGGGGCCAAT 660  
QY 661 GTGCATGCCCGGCGCTGCGGCGCTTCTTCCAGAGGCCCAAGGAGTCTCTTTTATTTTC 720  
DB 661 GTGCATGCCCGGCGCTGCGGCGCTTCTTCCAGAGGCCCAAGGAGTCTCTTTTATTTTC 720

QY 721 GGTGAGCTACCCCTCTCTTTGGCCGCTTGACCAAGCAGTGGGATGTGTAACTACCTC 780  
 Db 721 GGTGAGCTACCCCTCTCTTTGGCCGCTTGACCAAGCAGTGGGATGTGTAACTACCTC 780  
 QY 781 CTGGAGAAACCAACACAGCCCGCAGCCTGACGGCCACTGACTCCAGGGCAACACAGTC 840  
 Db 781 CTGGAGAAACCAACACAGCCCGCAGCCTGACGGCCACTGACTCCAGGGCAACACAGTC 840  
 QY 841 CTGCATGCCCTAGTGATGATCTCGACAACTCAGCTGAGAAATTTGCACTGTGTGACACAGC 900  
 Db 841 CTGCATGCCCTAGTGATGATCTCGACAACTCAGCTGAGAAATTTGCACTGTGTGACACAGC 900  
 QY 901 ATGTATGATGGGCTCTCAAGCTGGGGCCCGCTCTGSCCTACCTGACGCTTGAGGAC 960  
 Db 901 ATGTATGATGGGCTCTCAAGCTGGGGCCCGCTCTGSCCTACCTGACGCTTGAGGAC 960  
 QY 961 ATCCGCAACTGACAGGATCTCAGCCCTCTGAAGCTGGCCGCGCAAGGAGGCAAGATCGAG 1020  
 Db 961 ATCCGCAACTGACAGGATCTCAGCCCTCTGAAGCTGGCCGCGCAAGGAGGCAAGATCGAG 1020  
 QY 1021 ATTTTCAGGCACATCTGACAGCGGAGTTTTCAGGACTGAGCCACTTTTCCGAAAGTTTC 1080  
 Db 1021 ATTTTCAGGCACATCTGACAGCGGAGTTTTCAGGACTGAGCCACTTTTCCGAAAGTTTC 1080  
 QY 1081 ACCGAGTGTGCTATGGGCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGTGGACAGC 1140  
 Db 1081 ACCGAGTGTGCTATGGGCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGTGGACAGC 1140  
 QY 1141 TGTGAGGAGAACTCAGTGTGAGATCATTTGCCCTTTTCAATGCAAGAGCCGCAACGACAC 1200  
 Db 1141 TGTGAGGAGAACTCAGTGTGAGATCATTTGCCCTTTTCAATGCAAGAGCCGCAACGACAC 1200  
 QY 1201 CGAATGGTGGTTTGGAGCCCTGAAACAACTGCTGAGCGCGAAGTGGGATCTGCTCATC 1260  
 Db 1201 CGAATGGTGGTTTGGAGCCCTGAAACAACTGCTGAGCGCGAAGTGGGATCTGCTCATC 1260  
 QY 1261 CCCAAGTTCTTAACTTCCTGTGATCTGATCTACATGTTCTATCTTCAACGCTGTT 1320  
 Db 1261 CCCAAGTTCTTAACTTCCTGTGATCTGATCTACATGTTCTATCTTCAACGCTGTT 1320  
 QY 1321 GCCTACCATCAGCTTACCTTGAAGAGAGCGCCGCTTCACTGAAAGCGAGGTTGGA 1380  
 Db 1321 GCCTACCATCAGCTTACCTTGAAGAGAGCGCCGCTTCACTGAAAGCGAGGTTGGA 1380  
 QY 1381 AACTCCATGCTGACAGGSCCACTCTTATCTGCTAGGGGGAATCTACCTCTCGTG 1440  
 Db 1381 AACTCCATGCTGACAGGSCCACTCTTATCTGCTAGGGGGAATCTACCTCTCGTG 1440  
 QY 1441 GGCCAGCTGTGTACTTCTGGCGGCCGACGCTGTTCTATCTGGATCTCGTTCTATAGACAGC 1500  
 Db 1441 GGCCAGCTGTGTACTTCTGGCGGCCGACGCTGTTCTATCTGGATCTCGTTCTATAGACAGC 1500  
 QY 1501 TACTTTGAAATCCTCTTCTGTGTTCCAGGCGCTGCTCACAGTGGTGTCCAGGTTGCTGT 1560  
 Db 1501 TACTTTGAAATCCTCTTCTGTGTTCCAGGCGCTGCTCACAGTGGTGTCCAGGTTGCTGT 1560  
 QY 1561 TTCTGGCCATCAGTGTGTAACCTGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
 Db 1561 TTCTGGCCATCAGTGTGTAACCTGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
 QY 1621 AACTGCTTTACTATACAGTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAG 1680  
 Db 1621 AACTGCTTTACTATACAGTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAG 1680  
 QY 1681 AAGGTCACTCTGGGACCTGCTGGCTTCTGATCTTACTTACTTCTTCTTCTTCTTCTGGC 1740  
 Db 1681 AAGGTCACTCTGGGACCTGCTGGCTTCTGATCTTACTTACTTCTTCTTCTTCTTCTGGC 1740  
 QY 1741 TTCTGCTGTAGCCTGTGAGCCTGAGCCAGGAGGCTTGGCCCGGCAAGCTCTCTACAGGC 1800  
 Db 1741 TTCTGCTGTAGCCTGTGAGCCTGAGCCAGGAGGCTTGGCCCGGCAAGCTCTCTACAGGC 1800  
 QY 1801 CCCAATGCCACAGAGTCAAGTGACCCATCGAGGGGACAGGAGGACGAGGGCAACGGGGCC 1860

Db 1801 CCCAATGCCACAGAGTCAAGTGACCCATGAGGGACAGAGGCAACGGGGCC 1860  
 QY 1861 CAGTACAGGGGTATCCTGGAAGCCTCTTGGAGCTCTTCAAATTCACCATCGGCATGGGC 1920  
 Db 1861 CAGTACAGGGGTATCCTGGAAGCCTCTTGGAGCTCTTCAAATTCACCATCGGCATGGGC 1920  
 QY 1921 GAGCTGGCTTCCAGGAGCAGTGCATTTCCGGGCATGGTCTGCTGCTGCTGCTG 1980  
 Db 1921 GAGCTGGCTTCCAGGAGCAGTGCATTTCCGGGCATGGTCTGCTGCTGCTGCTG 1980  
 QY 1981 TACGTGCTGCTCACCTACATCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACC 2040  
 Db 1981 TACGTGCTGCTCACCTACATCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACC 2040  
 QY 2041 GTCAAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCAAGAAAGCCATCTCTGTC 2100  
 Db 2041 GTCAAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCAAGAAAGCCATCTCTGTC 2100  
 QY 2101 CTGGAGATGGAGAAATGGCTATTGGTGTGAGGAGAGCAGCGGCGAGGTGTGATGCTG 2160  
 Db 2101 CTGGAGATGGAGAAATGGCTATTGGTGTGAGGAGAGCAGCGGCGAGGTGTGATGCTG 2160  
 QY 2161 ACCGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGCTTCAAGGCTGGAGGAG 2220  
 Db 2161 ACCGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGCTTCAAGGCTGGAGGAG 2220  
 QY 2221 GTGAACTGGGCTTCAATGGAGCAGACGCTGCTACGCTGTGTGAGGACCCGTCAGGGGCA 2280  
 Db 2221 GTGAACTGGGCTTCAATGGAGCAGACGCTGCTACGCTGTGTGAGGACCCGTCAGGGGCA 2280  
 QY 2281 GGTGTCCCTCGAAGCTCTCGAGAACCTGCTGCTGGCTTCCCTCCAGAGGAGATGAGGAT 2340  
 Db 2281 GGTGTCCCTCGAAGCTCTCGAGAACCTGCTGCTGGCTTCCCTCCAGAGGAGATGAGGAT 2340  
 QY 2341 GGTGCTCTGAGGAAACTATGTGCCCTGTCAGCTCTCCAGTCCCACTGATGGCCGACA 2400  
 Db 2341 GGTGCTCTGAGGAAACTATGTGCCCTGTCAGCTCTCCAGTCCCACTGATGGCCGACA 2400  
 QY 2401 TGCAGAGAGGAGCCAGAGACAGAGCAGAGGATCTTTCCACCAACATCTGCTGGCTCTGG 2460  
 Db 2401 TGCAGAGAGGAGCCAGAGACAGAGCAGAGGATCTTTCCACCAACATCTGCTGGCTCTGG 2460  
 QY 2461 GGTCCCACT 2469  
 Db 2461 GGTCCCACT 2469

RESULT 3

AAA30254  
 ID AAA30254 standard; cDNA; 2809 BP.

XX

AC AAA30254;

XX

DT 05-SEP-2000 (first entry)

XX

DE Human VR-2 coding sequence.

XX

KW VR-2; human; vanilloid receptor; nociceptor; pain signalling;  
 hyperalgesia; musculoskeletal disorder; neuropathic pain;  
 chromosome 17p11-12; gene therapy; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 361..2655

FT /\*tag= a

FT /product= "VR-2"

FT /note= "This region is specifically claimed"

XX

PN WO200029577-A1.

XX

PD 25-MAY-2000.

XX 12-NOV-1999; 99WO-US026701.  
 XX PF 13-NOV-1998; 98US-0108322P.  
 XX PR 28-DEC-1998; 98US-0114078P.  
 PR 26-FEB-1999; 99US-00258633.  
 PR 19-OCT-1999; 99US-00421134.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Curtis RAJ;  
 XX WPI; 2000-387790/33.  
 XX P-PSDB; AAY97358.  
 XX New capsaicin/vanilloid receptor polynucleotides and polypeptides, used  
 PT to modulate pain signaling mechanisms.  
 XX Claim 1; Fig 2; 183pp; English.  
 XX The present sequence is the coding sequence for human capsaicin/vanilloid  
 CC receptor VR-2, which is involved in pain signaling. The sequence was  
 CC isolated by searching a heart library for genes encoding novel receptors  
 CC of the capsaicin/vanilloid family, and has been shown to be located at  
 CC chromosome 17p11-12. This region has been associated with myasthenia  
 CC gravis, Smith-Magenis syndrome, CORD5, Cone-rod dystrophy, choroidal  
 CC dystrophy, central areolar and retinal cone dystrophy, and it is possible  
 CC that the protein may be used to treat or diagnose these disorders. In  
 CC addition, the gene, protein and its antibodies can be used to diagnose  
 CC and treat hyperalgesia, inflammation, infection, ischaemia, joint pain,  
 CC tooth pain, headaches, pain associated with surgery or neuropathic pain,  
 CC possibly via the use of gene therapy  
 XX  
 SQ Sequence 2809 BP; 601 A; 825 C; 798 G; 585 T; 0 U; 0 Other;  
 Query Match 99.7%; Score 2462.2; DB 3; Length 2809;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2464; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 3 CGAGGCGGCGCGAGCTGGGAGGAGAGACAGGACCCCTTGACATCTCGATCTGCACAGAGG 62  
 267 CAACACCGACGCGCAGCTGGGAGGAGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG 326  
 63 TCCTGGCTGACGAGCGAGCTCTCTCTCTAGATGACCTCACCTCCAGCTCTCCAGT 122  
 327 TCCTGGCTGACGAGCGAGCTCTCTCTCTAGATGACCTCACCTCCAGCTCTCCAGT 386  
 123 TTTTCAGGTTGGAGACATTAGATGGAGGCGGAGGAGATGGCTCTGAGGCGGACAGAGGAAA 182  
 387 TTTTCAGGTTGGAGACATTAGATGGAGGCGGAGGAGATGGCTCTGAGGCGGACAGAGGAAA 446  
 183 GCTGGATTTTGGAGCGGGCTGCTCCATGGAGTCAAGTTCAGGCGGAGGAGCGGAAA 242  
 447 GCTGGATTTTGGAGCGGGCTGCTCCATGGAGTCAAGTTCAGGCGGAGGAGCGGAAA 506  
 243 ATTGCGCCCTCAGATAGAGTCAACCTCACTACCGAAAGGAGGAGTCCAGTCAAGCC 302  
 507 ATTGCGCCCTCAGATAGAGTCAACCTCACTACCGAAAGGAGGAGTCCAGTCAAGCC 566  
 303 GGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTGTCCCGGA 362  
 567 GGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTGTCCCGGA 626  
 363 GGATCTGGCTGGATTTCCAGAGTACCTGAGCAGACAGCAGCAGTACCTACCGACTCGGA 422  
 627 GGATCTGGCTGGATTTCCAGAGTACCTGAGCAGACAGCAGCAGTACCTACCGACTCGGA 686  
 423 ATACACAGAGGGCTCCACAGGTAGAGTGCCTGATGAGGCTGTGCTGAACCTTAAGGA 482  
 687 ATACACAGAGGGCTCCACAGGTAGAGTGCCTGATGAGGCTGTGCTGAACCTTAAGGA 746  
 483 CGGAGTCAATGCTGCAATTTGCGCACTGTGCGAGATCGACAGGGAGCTCTGGCAATCTCTCA 542

Db 747 CGAGTCAATGCTGCAATTTCTGCCACTGCTGCAGATCGACAGGAGCTCTGGCAATCCTCA 806  
 QY 543 GCCCTCTGTTAAATGCCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCACAT 602  
 Db 807 GCCCTCTGTTAAATGCCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCACAT 866  
 QY 603 CGCCATTGAGAAAGAGAGTCTGCACTGTGTAAGCTCTCTGTTGGAGAAATGGGCGCAATGT 662  
 Db 867 CGCCATTGAGAAAGAGAGTCTGCACTGTGTAAGCTCTCTGTTGGAGAAATGGGCGCAATGT 926  
 QY 663 GCATGCCCGGCGCTGGGCGCGCTTCTCCAGAAAGGSCCAAGGAGTCTGCTTTTATTTCGG 722  
 Db 927 GCATGCCCGGCGCTGGGCGCGCTTCTCCAGAAAGGSCCAAGGAGTCTGCTTTTATTTCGG 986  
 QY 723 TGAGCTACCCCTCTCTTTTGGCGCGCTTGCAACCAAGCAGTGGGATGTGTAAGCTACCTCCT 782  
 Db 987 TGAGCTACCCCTCTCTTTGGCGCGCTTGCAACCAAGCAGTGGGATGTGTAAGCTACCTCCT 1046  
 QY 783 GGAGAAACCCACACCGAGCGCGCTGCGAGCCACTGACTCCAGGGGCAACACAGTCTCT 842  
 Db 1047 GGAGAAACCCACACCGAGCGCGCTGCGAGCCACTGACTCCAGGGGCAACACAGTCTCT 1106  
 QY 843 GCATGCCCTAGTGTGATCTCGGACAACTCAGCTGAGAACATTGCACTGTGTGACCAAGCAT 902  
 Db 1107 GCATGCCCTAGTGTGATCTCGGACAACTCAGCTGAGAACATTGCACTGTGTGACCAAGCAT 1166  
 QY 903 GTATGATGGGCTCTCTCAAGCTGGGCGCGCTCTGCTCCCTACCGTGCAGCTTGAGGACAT 962  
 Db 1167 GTATGATGGGCTCTCTCAAGCTGGGCGCGCTCTGCTCCCTACCGTGCAGCTTGAGGACAT 1226  
 QY 963 CGCGAACTGTCAGGATCTCAAGCTGTGAAAGCTGGCGCGCAAGGAGGGCAAGATCGAGAT 1022  
 Db 1227 CGCGAACTGTCAGGATCTCAAGCTGTGAAAGCTGGCGCGCAAGGAGGGCAAGATCGAGAT 1286  
 QY 1023 TTTTCAGGACATCTGTCAGCGGGAGTTTTCAGGACTGAGCCACCTTTCCCGAAGTTTCAC 1082  
 Db 1287 TTTTCAGGACATCTGTCAGCGGGAGTTTTCAGGACTGAGCCACCTTTCCCGAAGTTTCAC 1346  
 QY 1083 CGAGTGGTCTATGGGCTCTGCGGCTGTGCTGTATGACCTGGCTCTGTGTGACAGCTG 1142  
 Db 1347 CGAGTGGTCTATGGGCTCTGCGGCTGTGCTGTATGACCTGGCTCTGTGTGACAGCTG 1406  
 QY 1143 TGAGGAGAACTCAGTGTGAGATCAATGCTTTTCAATGCAAGAGCGCGCACCGACACCG 1202  
 Db 1407 TGAGGAGAACTCAGTGTGAGATCAATGCTTTTCAATGCAAGAGCGCGCACCGACACCG 1466  
 QY 1203 AATGTCGTTTGGAGCGCTTGAACAACTGCTGCGAGGGGAAATGGATCTGCTCATCCC 1262  
 Db 1467 AATGTCGTTTGGAGCGCTTGAACAACTGCTGCGAGGGGAAATGGATCTGCTCATCCC 1326  
 QY 1263 CAAGTCTCTTAAACTTCTGTGTAATCTGATCTACATGTTTCACTTCAACCGCTGTTCG 1322  
 Db 1527 CAAGTCTCTTAAACTTCTGTGTAATCTGATCTACATGTTTCACTTCAACCGCTGTTCG 1586  
 QY 1323 CTACCATCAGCCTTACCTTGAAGAGCAGGCGCGCTTCACTGAAAGCGGAGGTTGGAAA 1382  
 Db 1587 CTACCATCAGCCTTACCTTGAAGAGCAGGCGCGCTTCACTGAAAGCGGAGGTTGGAAA 1646  
 QY 1383 CTCCTGCTGCTGACCGGCGCACTCTTATCTCTGCTAGGGGGATCTACCTCTCTCGTGG 1442  
 Db 1647 CTCCTGCTGCTGACCGGCGCACTCTTATCTCTGCTAGGGGGATCTACCTCTCTCGTGG 1706  
 QY 1443 CCAGCTGTGTACTTCTGCGGCGCCACGCTGTTTCACTTGGATCTCGTTCATAGACAGCTA 1502  
 Db 1707 CCAGCTGTGTACTTCTGCGGCGCCACGCTGTTTCACTTGGATCTCGTTCATAGACAGCTA 1766  
 QY 1503 CTTTGAATCTCTCTTCTGTTCCAGGCGCTGCTCAAGTGGTGTCCAGGCTGTGTGTTT 1562  
 Db 1767 CTTTGAATCTCTCTTCTGTTCCAGGCGCTGCTCAAGTGGTGTCCAGGCTGTGTGTTT 1826  
 QY 1563 CTTGGCGCATCGAGTGTGATCTGCGCTGCTGTTGTTGCTGCGCTGCTGGCTGGCTGAA 1622  
 Db 1827 CTTGGCGCATCGAGTGTGATCTGCGCTGCTGTTGTTGCTGCGCTGCTGGCTGGCTGAA 1886

QY	1623	CCTGCTTTACTATACACGTGGCTTCCAGACACAGGCACTACAGTGTCAATGATCAGAA	1682
Db	1887	CCTGCTTTACTATACACGTGGCTTCCAGACACAGGCACTACAGTGTCAATGATCAGAA	1946
QY	1683	GGTCATCCTGGGGACCTGCTGGCTTCCCTGATCTACTTAGTCTCTCTTTGGCTT	1742
Db	1947	GGTCATCCTGGGGACCTGCTGGCTTCCCTGATCTACTTAGTCTCTCTTTGGCTT	2006
QY	1743	CGCTGTAGCCCTGGTGAGCCTGAGCCAGGAGGCTTGGCGCCCGAAAGCTCCTACAGCCCC	1802
Db	2007	CGCTGTAGCCCTGGTGAGCCTGAGCCAGGAGGCTTGGCGCCCGAAAGCTCCTACAGCCCC	2066
QY	1803	CAATGCCACAGAGTCACTGAGCCCATGAGGAGACAGAGGCAAGGGGCCCA	1862
Db	2067	CAATGCCACAGAGTCACTGAGCCCATGAGGAGACAGAGGCAAGGGGCCCA	2126
QY	1863	GTACAGGGGTATCCTGGAGCCCTCTTGGAGCTCTTCAAATTCACCATCGGCATGGCGA	1922
Db	2127	GTACAGGGGTATCCTGGAGCCCTCTTGGAGCTCTTCAAATTCACCATCGGCATGGCGA	2186
QY	1923	GCTGGCTTCCAGGACAGCTGCACCTTCCGCGCATGTGTCTGCTGCTGCGCCTA	1982
Db	2187	GCTGGCTTCCAGGACAGCTGCACCTTCCGCGCATGTGTCTGCTGCTGCGCCTA	2246
QY	1983	CGTGTGCTCACTACATCTGCTCAATGCTCAATGCTCAATGCTCAATGCTCAATGCT	2042
Db	2247	CGTGTGCTCACTACATCTGCTCAATGCTCAATGCTCAATGCTCAATGCTCAATGCT	2306
QY	2043	CACAGTGTGCGCCTGACAGCTGAGCATCTGGAAGCTGCAAGAGCCATCTCTGCTCT	2102
Db	2307	CACAGTGTGCGCCTGACAGCTGAGCATCTGGAAGCTGCAAGAGCCATCTCTGCTCT	2366
QY	2103	GGAGATGGAAATGGCTATTGGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG	2162
Db	2367	GGAGATGGAAATGGCTATTGGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG	2426
QY	2163	CGTTGGCACTAAGCCAGATGGAGCCCGGATGAGCGCTGGTTCAGGGTGAGAGGT	2222
Db	2427	CGTTGGCACTAAGCCAGATGGAGCCCGGATGAGCGCTGGTTCAGGGTGAGAGGT	2486
QY	2223	GAACTGGCTTATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2282
Db	2487	GAACTGGCTTATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2546
QY	2283	TGTCCTCTCGAACTCTCGAGAACCTCTGCTGGCTTCCCTCCCAAGGAGATGAGATGG	2342
Db	2547	TGTCCTCTCGAACTCTCGAGAACCTCTGCTGGCTTCCCTCCCAAGGAGATGAGATGG	2606
QY	2343	TGCTCTGAGGAAAATATGTGCGCGTCCAGTCTCCAGTCCCACTGATGGCCAGATG	2402
Db	2607	TGCTCTGAGGAAAATATGTGCGCGTCCAGTCTCCAGTCCCACTGATGGCCAGATG	2666
QY	2403	CAGCAGGAGCCAGAGACAGAGAGAGATCTTCCACACCATCTGCTGGCTCTGGGG	2462
Db	2667	CAGCAGGAGCCAGAGACAGAGAGATCTTCCACACCATCTGCTGGCTCTGGGG	2726
QY	2463	TCCCACT 2469	
Db	2727	TCCCACT 2733	
RESULT 4			
ID	ADQ89073	standard; cDNA; 2809 BP.	
XX	AC	ADQ89073;	
XX	XX	21-OCT-2004 (first entry)	
DE	DE	Human urological disorder related protein 18560 encoding cDNA SEQ.25.	
XX	XX	urological disorder; uropathic; cytostatic; urinary incontinence;	

KW	benign prostatic hyperplasia; human; gene; ss.
XX	Homo sapiens.
XX	Key
FT	Location/Qualifiers
FT	361..2655
FT	/*tag= a
FT	/product= "urological disorder related protein 18560"
XX	WO2004065576-A2.
PN	05-AUG-2004.
XX	14-JAN-2004; 2004WO-US000750.
XX	15-JAN-2003; 2003US-0440318P.
PR	04-FEB-2003; 2003US-0444783P.
PR	27-MAR-2003; 2003US-0457901P.
PR	08-MAY-2003; 2003US-0468775P.
PR	19-MAY-2003; 2003US-0471614P.
PR	16-JUN-2003; 2003US-0478742P.
PR	18-JUL-2003; 2003US-0488529P.
PR	30-JUL-2003; 2003US-0491156P.
PR	02-SEP-2003; 2003US-049594P.
PR	26-SEP-2003; 2003US-0506332P.
XX	(MILL-) MILLENNIUM PHARM INC.
XX	Karicheti V, Silos-Santiago I, Eliasof SD;
XX	WPI; 2004-562167/54.
DR	P-PSDB; AD089074.
XX	Use of polypeptides related to urological disorders, e.g. 44390, 54181, 211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological disorder.
XX	Claim 1; SEQ ID NO 25; 542pp; English.
XX	The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder. The compound has uropathic and cytostatic activities. The polypeptides related to urological disorders are useful for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Disorders include urinary incontinence and benign prostatic hyperplasia. The present sequence encodes a human urological disorder related protein, which is used in the exemplification of the present invention.
XX	Sequence 2809 BP; 601 A; 825 C; 798 G; 585 T; 0 U; 0 Other;
QY	Query Match 99.7%; Score 2462.2; DB 13; Length 2809;
Db	Best Local Similarity 99.9%; Pred. No. 0;
QY	Matches 2464; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db	3 CGAGGCCGACCGCGAGCTGGAGGAGAGACAGGACCCCTGACATCTCCATCTGCACAGG 62
QY	267 CAACACCGACCGCGAGCTGGAGGAGAGACAGGACCCCTTGACATCTCCATCTGCACAGG 326
Db	63 TCCTGGCTGGACCGGAGCAGCTCTCTCTAGGATGACCTCACCCCTCCAGCTCTCCAGT 122
QY	327 TCCTGGCTGGACCGGAGCAGCTCTCTCTAGGATGACCTCACCCCTCCAGCTCTCCAGT 386
Db	123 TTTTCAGGTTGGAGACATTAGATGGAGGCCAAGAAGATGGCTCTGAGCGCGACAGAGAAA 182
QY	387 TTTTCAGGTTGGAGACATTAGATGGAGGCCAAGAAGATGGCTCTGAGCGCGACAGAGAAA 446



QY	183	GCTGGATTTTGGAGCGGGTGCTCCCTCCATGGAGTCAAGTTCCAGGGGAGGACCGGAA	242	1263	CAAGTTCTTTAAATCTTCTGTGTAATCTGAATCTACATGTTCACTTCAACGGCTTTGC	1322
Db	447	GCTGGATTTTGGAGCGGGTGCTCCCTCCATGGAGTCAAGTTCCAGGGGAGGACCGGAA	506	1527	CAAGTTCTTTAAATCTTCTGTGTAATCTGAATCTACATGTTCACTTCAACGGCTTTGC	1586
QY	243	ATTGCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAGGGAAAGGTGCCAGTCAAGCC	302	1323	CTACCATCAGCCCTACCTGAAAGAGGAGCGGCCCTCACTGAAAGCGGAGGTTGGAAA	1382
Db	507	ATTGCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAGGGAAAGGTGCCAGTCAAGCC	566	1587	CTACCATCAGCCCTACCTGAAAGAGGAGCGGCCCTCACTGAAAGCGGAGGTTGGAAA	1646
QY	303	GGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCGA	362	1383	CTCCATGCTGCTGACGGGGCCACATCCTTATCTCTGTAGGGGGGATCTACCTCTCGTGGG	1442
Db	567	GGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCGA	626	1647	CTCCATGCTGCTGACGGGGCCACATCCTTATCTCTGTAGGGGGGATCTACCTCTCGTGGG	1706
QY	363	GGATCTGGCTGGACTTCCAGAGTACCTGACGAGACCCAGCAAGTACTCAACCGACTCGGA	422	1443	CCAGCTGTGGTACTTCTGGCGGCGCCACGCTGTTCATCTGGATCTCGTTTATAGACAGCTA	1502
Db	627	GGATCTGGCTGGACTTCCAGAGTACCTGACGAGACCCAGCAAGTACTCAACCGACTCGGA	686	1707	CCAGCTGTGGTACTTCTGGCGGCGCCACGCTGTTCATCTGGATCTCGTTTATAGACAGCTA	1766
QY	423	ATACACAGAGGGCTCCACAGTAAGAGTGCCTCTGATGAAGGCTGTGCTGAACCTTAAAGGA	482	1503	CTTTGAAATCCTTCTCTGTTCCAGGCCCTGCTCAAGTGGTGTCCAGGCTGTGTGTTT	1562
Db	687	ATACACAGAGGGCTCCACAGTAAGAGTGCCTCTGATGAAGGCTGTGCTGAACCTTAAAGGA	746	1767	CTTTGAAATCCTTCTCTGTTCCAGGCCCTGCTCAAGTGGTGTCCAGGCTGTGTGTTT	1826
QY	483	CGAGTCAATGCTGCTGCAATCTTGCCACTGCTGCGAGATCGACAGGACTCTGGGCAATCCTCA	542	1563	CTTGGCCATCGAGTGTACTGCCCCCTGCTTGTGTCTGGCTGGTGTCTGGGCTGGGCTGAA	1622
Db	747	CGAGTCAATGCTGCTGCAATCTTGCCACTGCTGCGAGATCGACAGGACTCTGGGCAATCCTCA	806	1827	CTTGGCCATCGAGTGTACTGCCCCCTGCTTGTGTCTGGCTGGTGTCTGGGCTGGGCTGAA	1886
QY	543	GCCCCCTGTAATGCCAGTGCCACAGATGACTATTACCGAGGCCACAGCGCTCTGCACAT	602	1623	CCTGCTTTTACTATACACGTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAGAA	1682
Db	807	GCCCCCTGTAATGCCAGTGCCACAGATGACTATTACCGAGGCCACAGCGCTCTGCACAT	866	1887	CCTGCTTTTACTATACACGTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAGAA	1946
QY	603	CGCCATTGAGAAGAGGAGTCTGCAGTGTGTGAAGCTCTCTGGTGAGAAATGGGGCCAAATGT	662	1683	GGTCATCTCGGGGACTCTGCTGGCTTCTCTCTGATCTACTTACTTCTTCTTCTTCTTCTTCTT	1742
Db	867	CGCCATTGAGAAGAGGAGTCTGCAGTGTGTGAAGCTCTCTGGTGAGAAATGGGGCCAAATGT	926	1947	GGTCATCTCGGGGACTCTGCTGGCTTCTCTCTGATCTACTTACTTCTTCTTCTTCTTCTTCTT	2006
QY	663	GCATGCCCGGGCTGCGGGCGCTTCTTCCAGAGGGCCAAAGGACTTGTCTTTTATTTTCGG	722	1743	CGCTGTAGCCCTGTGAGCCTGAGCCAGGAGGCTTGGCGCCCCGAAAGCTCCTACAGGCC	1802
Db	927	GCATGCCCGGGCTGCGGGCGCTTCTTCCAGAGGGCCAAAGGACTTGTCTTTTATTTTCGG	986	2007	CGCTGTAGCCCTGTGAGCCTGAGCCAGGAGGCTTGGCGCCCCGAAAGCTCCTACAGGCC	2066
QY	723	TGAGTACCCCTCTCTTTTGGCGGCTTGCAACAGAGTGGGATGTGTAAGTACCTCTCT	782	1803	CAATGCCACAGAGTCTAGTGCAGCCATGAGGAGGACAGGAGGACAGGGGCAACGGGGCCCA	1862
Db	987	TGAGTACCCCTCTCTTTTGGCGGCTTGCAACAGAGTGGGATGTGTAAGTACCTCTCT	1046	2067	CAATGCCACAGAGTCTAGTGCAGCCATGAGGAGGACAGGAGGACAGGGGCAACGGGGCCCA	2126
QY	783	GGAGAACCCACACAGCCCGCCAGCTGCGAGGCCACTGACTCCCGAGGGCAACACAGTCTCT	842	1863	GTAACGGGTATCTGGAAGCCTCTTGGAGCTCTTCAATTCACCATCGGCAATGGGCGA	1922
Db	1047	GGAGAACCCACACAGCCCGCCAGCTGCGAGGCCACTGACTCCCGAGGGCAACACAGTCTCT	1106	2127	GTAACGGGTATCTGGAAGCCTCTTGGAGCTCTTCAATTCACCATCGGCAATGGGCGA	2186
QY	843	GCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAAATGTCATCTGGTGACAGCAT	902	1923	GCTGGCTCTTCCAGAGCAGCTGCATTTCCGCGCATGGTGTCTGCTGTCTGTCTGGGCTTA	1982
Db	1107	GCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAAATGTCATCTGGTGACAGCAT	1166	2187	GCTGGCTCTTCCAGAGCAGCTGCATTTCCGCGCATGGTGTCTGCTGTCTGTCTGGGCTTA	2246
QY	903	GTATGATGGGCTCTTCCAGCTGGGGCGGCTCTGCTGCTACCGTGCAGCTTGGAGCAT	962	1983	CGTGTGCTCACCCTACATCCTGCTGCTCAAATGCTCATCGCCCTCATGAGCGAGACCGT	2042
Db	1167	GTATGATGGGCTCTTCCAGCTGGGGCGGCTCTGCTGCTACCGTGCAGCTTGGAGCAT	1226	2247	CGTGTGCTCACCCTACATCCTGCTGCTCAAATGCTCATCGCCCTCATGAGCGAGACCGT	2306
QY	963	CCGCAACTGACGATCTCAGCCCTCTGAAAGCTGGCGCCCAAGGAGGGCAAGATCCGAGAT	1022	2043	CAAACAGTGTCCCACTGACAGCTGGAAGCATCTGGAAGCTCGAGAAAGCCATCTGTCTCT	2102
Db	1227	CCGCAACTGACGATCTCAGCCCTCTGAAAGCTGGCGCCCAAGGAGGGCAAGATCCGAGAT	1286	2307	CAAACAGTGTCCCACTGACAGCTGGAAGCATCTGGAAGCTCGAGAAAGCCATCTGTCTCT	2366
QY	1023	TTTCAGGCACATCTCTGACGGGAGTTTTCAGGACTGAGCCACTTTTCCGGAAGTTTCAC	1082	2103	GGAGATGGAGATGGCTATTGGTGGTGCAGGAAGACAGCGGCGAGTGTGATGCTGAC	2162
Db	1287	TTTCAGGCACATCTCTGACGGGAGTTTTCAGGACTGAGCCACTTTTCCGGAAGTTTCAC	1346	2367	GGAGATGGAGATGGCTATTGGTGGTGCAGGAAGACAGCGGCGAGTGTGATGCTGAC	2426
QY	1083	CGAGTGTGCTATGGGCTGTGCGGGTGTGCTGTATGACTGGCTTCTGTGGACAGCTG	1142	2163	CGTGTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGTGTCTTACGGGTGGAGGAGT	2222
Db	1347	CGAGTGTGCTATGGGCTGTGCGGGTGTGCTGTATGACTGGCTTCTGTGGACAGCTG	1406	2427	CGTGTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGTGTCTTACGGGTGGAGGAGT	2486
QY	1143	TGAGGAGAACTCAGTGTGGAGATCATTTGCTCTTTCATTGCAAGAGCCCGACACACCG	1202	2223	GAACTGGCTTCAATGGAGCAGAGCTGCTGCTTACGCTGTGTGAGGACCCGCTCAGGGGCGG	2282
Db	1407	TGAGGAGAACTCAGTGTGGAGATCATTTGCTCTTTCATTGCAAGAGCCCGACACACCG	1466	2487	GAACTGGCTTCAATGGAGCAGAGCTGCTGCTTACGCTGTGTGAGGACCCGCTCAGGGGCGG	2546
QY	1203	AATGGTCGTTTGGAGCCCTTGAAACAACTGCTCGAGCGGAAATGGGATCTGCTCATCCC	1262	2283	TGTCCTCTCGAACTCTCGAGAACCTGTCTCTGGCTTCCCTCCCAAGGAGATGAGGATGG	2342
Db	1467	AATGGTCGTTTGGAGCCCTTGAAACAACTGCTCGAGCGGAAATGGGATCTGCTCATCCC	1526	2547	TGTCCTCTCGAACTCTCGAGAACCTGTCTCTGGCTTCCCTCCCAAGGAGATGAGGATGG	2606
				2343	TGCTCTGAGGAAAACTATGTGCGCGCTCCAGCTCTCCAGTCTCCAACTGATGGGCCAGATG	2402

Db 2607 TGGCTCTGAGGAAATATGTGCGCTCCAGCTCTCCAGTCCACTGATGSCCAGATG 2666  
QY 2403 CAGCAGAGGCCAGAGGACAGAGCAGAGGATCTTTCCAAACCAATCTGCTGGCTTGGGG 2462  
Db 2667 CAGCAGAGGCCAGAGGACAGAGCAGAGGATCTTTCCAAACCAATCTGCTGGCTTGGGG 2726  
QY 2463 TCCCACT 2469  
Db 2727 TCCCACT 2733

RESULT 5  
ADQ83962  
ID ADQ83962 standard; cDNA; 2774 BP.  
XX AC ADQ83962;  
XX DT 07-OCT-2004 (first entry)  
XX Human tumour-associated antigenic target (TAT) cDNA sequence #776.  
XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
XX cancer; cell proliferative disorder; gene; ss.  
XX Homo sapiens.  
XX WO2004060270-A2.  
XX 22-JUL-2004.  
XX 15-OCT-2003; 2003WO-US029126.  
XX 18-OCT-2002; 2002US-0418988P.  
XX (GETH ) GENENTECH INC.  
XX (WUTD/) WU T D.  
XX (ZHOU/) ZHOU Y.  
XX Wu TD, Zhou Y;  
XX WPI; 2004-534300/51.  
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,  
XX preventing or treating cell proliferative disorders such as cancer.  
XX Claim 1; SEQ ID NO 776; 5504pp; English.

XX The present invention describes an isolated tumour-associated antigenic  
XX target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
XX sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
XX (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
XX sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
XX (c). Also described: (1) an expression vector comprising the above  
XX nucleic acid; (2) a host cell comprising the above expression vector; (3)  
XX a process for producing a polypeptide; (4) an isolated polypeptide  
XX comprising: (a) an amino acid sequence encoded by any of the above  
XX nucleotide sequences; (b) an amino acid sequence encoded by the full-  
XX length coding region of the above nucleotide sequences; or (c) a sequence  
XX having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
XX comprising the above polypeptide fused to a heterologous polypeptide; (6)  
XX an isolated antibody that binds to the above polypeptide; (7) a process  
XX for producing the antibody; (8) an isolated oligopeptide that binds to  
XX the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
XX binding organic molecule that binds to the above polypeptide; (10) a  
XX composition of matter comprising the above (chimeric) polypeptide,  
XX antibody, oligopeptide or TAT binding organic molecule, in combination  
XX with a carrier; (11) an article of manufacture comprising a container and  
XX the composition of matter contained within the container; (12) methods of  
XX inhibiting the growth of a cell that expresses the above protein, where  
XX the growth of the cell is at least in part dependent upon a growth  
XX potentiating effect of the above protein; (13) a method of  
XX therapeutically treating a mammal having a cancerous tumour comprising

CC cells that express the above protein; (14) a method of determining the  
CC presence of a protein in a sample suspected of containing the protein  
CC described above; (15) methods of diagnosing the presence of a tumour in a  
CC mammal; (16) a method for treating or preventing a cell proliferative  
CC disorder associated with increased expression or activity of the above  
CC protein; and (17) a method of binding an antibody, oligopeptide or  
CC organic molecule to a cell that expresses the protein described above.  
CC The TAT sequences have cytostatic activities, and can be used in gene  
CC therapy. The composition and methods are useful for diagnosing, preparing  
CC preventing or treating cancer. The composition is also used for preparing  
CC a medicament for the therapeutic treatment or diagnostic detection of a  
CC cell proliferative disorder or cancer. The present sequence represents a  
CC human TAT cDNA sequence from the present invention.

XX  
SQ Sequence 2774 BP; 560 A; 827 C; 799 G; 588 T; 0 U; 0 Other;  
Query Match 99.7%; Score 2460.6; DB 13; Length 2774;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2463; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3 CGAGCCGACGCGCAGCTGGGAGGAGACAGACGACCTTGACATCTCCATCTGCACAGAG 62  
Db 274 CAACACCGACGCGCAGCTGGGAGGAGACAGACGACCTTGACATCTCCATCTGCACAGAG 333  
QY 63 TCCTGGCTGGACCGAGCAGCCTCTCTCTCTAGGATGACCTCACCTCCAGCTCTCCAGT 122  
Db 334 TCCTGGCTGGACCGAGCAGCCTCTCTCTCTAGGATGACCTCACCTCCAGCTCTCCAGT 393  
QY 123 TTTTCAAGTTGGAGACATTAGATGGAGGCGCAAGAGATGGCTCTGAGGCGGACAGAGAAA 182  
Db 394 TTTTCAAGTTGGAGACATTAGATGGAGGCGCAAGAGATGGCTCTGAGGCGGACAGAGAAA 453  
QY 183 GCTGATTTTGGAGGGGGCTGCTCCCATGAGTTCACATTTCCAGGGGAGGACCGGA 242  
Db 454 GCTGATTTTGGAGGGGGCTGCTCCCATGAGTTCACATTTCCAGGGGAGGACCGGA 513  
QY 243 ATTTGCGCCCTCAGATAAGAGTCAACTCACTACCGAAAGGAAACAGGTGCCAGTCAGCC 302  
Db 514 ATTTGCGCCCTCAGATAAGAGTCAACTCACTACCGAAAGGAAACAGGTGCCAGTCAGCC 573  
QY 303 GGATCCAAACCGATTTGACCGAGATGGCTCTTCAATCGGTCTCCCGGGGTGTCGCCGA 362  
Db 574 GGATCCAAACCGATTTGACCGAGATGGCTCTTCAATCGGTCTCCCGGGGTGTCGCCGA 633  
QY 363 GGATCTGGCTGACTTCCAGAGTACTCTGAGCAGACAGACAGACAGTACTCACCGACTCGGA 422  
Db 634 GGATCTGGCTGACTTCCAGAGTACTCTGAGCAGACAGACAGTACTCACCGACTCGGA 693  
QY 423 ATACACAGAGGGCTCCACAGGTAAAGACGTGCTGTGATGAAGGTGTGCTGAACTTAAGGA 482  
Db 694 ATACACAGAGGGCTCCACAGGTAAAGACGTGCTGTGATGAAGGTGTGCTGAACTTAAGGA 753  
QY 483 CGGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542  
Db 754 CGGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 813  
QY 543 GCGCTTGGTAAATGCGCCAGTGCAGATGACTTATACCGAGGCCACAGGCTCTGCACAT 602  
Db 814 GCGCTTGGTAAATGCGCCAGTGCAGATGACTTATACCGAGGCCACAGGCTCTGCACAT 873  
QY 603 CGCATTGAGAGAGAGAGTCTGAGTGTGTGAGTCTCTGCTGAGAGATGGGGCCCAATGT 662  
Db 874 CGCATTGAGAGAGAGAGTCTGAGTGTGTGAGTCTCTGCTGAGAGATGGGGCCCAATGT 933  
QY 663 GCATGCCCGGGCTCGGGCGCTTTTCCAGAGGGGCCAAGGACATTGCTTTTATTTTCGG 722  
Db 934 GCATGCCCGGGCTCGGGCGCTTTTCCAGAGGGGCCAAGGACATTGCTTTTATTTTCGG 993  
QY 723 TGAGCTACCCCTCTCTTTGGCGCTTGACACAGCAGTGGGATGTGTGAGTCTACCTCCT 782  
Db 994 TGAGCTACCCCTCTCTTTGGCGCTTGACACAGCAGTGGGATGTGTGAGTCTACCTCCT 1053  
QY 783 GGAGAACCCACACACAGCCCGCCAGCCTGCGAGGCCACTGACTCCCGAGGGCAACACAGTCTCT 842

1054 GGAAGACCCACACACGCGCCAGCTGCGAGCCACTGACTCCAGGGCAACACAGTCCT 1113  
 843 GCATGCCCTAGTATGATCTCGAACAACCTAGCTGAGAACATTGCTGATGACAGAT 902  
 1114 GCATGCCCTAGTATGATCTCGAACAACCTAGCTGAGAACATTGCTGATGACAGAT 1173  
 903 GTATGATGGGCTCCTCCAGCTGGGGCCGCGCTGCGCTTACCGTACAGCTTGCAGACAT 962  
 1174 GTATGATGGGCTCCTCCAGCTGGGGCCGCGCTGCGCTTACCGTACAGCTTGCAGACAT 1233  
 963 CCGCAACCTCGAGGATCTCAAGCTCTGAAAGCTGGCGCCCAAGAGGCGCAAGATCGAGAT 1022  
 1234 CCGCAACCTCGAGGATCTCAAGCTCTGAAAGCTGGCGCCCAAGAGGCGCAAGATCGAGAT 1293  
 1023 TTTTCAGGCAATCTCGAGCGGAGTTTTCAGGCTGAGGCACTTTTCCCGAAAGTTTCA 1082  
 1294 TTTTCAGGCAATCTCGAGCGGAGTTTTCAGGCTGAGGCACTTTTCCCGAAAGTTTCA 1353  
 1083 CGATGGTGTATGGGCTCTCGGGTGTGCTGTATGACTGCTGCTTCTGTGACAGCTG 1142  
 1354 CGATGGTGTATGGGCTCTCGGGTGTGCTGTATGACTGCTGCTTCTGTGACAGCTG 1413  
 1143 TGAGGAACTCAGTGTGAGATCATTTGCTTTTCAATTGCAAGAGCGCGCACCGACCG 1202  
 1414 TGAGGAACTCAGTGTGAGATCATTTGCTTTTCAATTGCAAGAGCGCGCACCGACCG 1473  
 1203 AATGGTCGTTTGGAGCCCTGAAACAACTGCTGAGCGGCAATGGGATCTGCTCATCCC 1262  
 1474 AATGGTCGTTTGGAGCCCTGAAACAACTGCTGAGCGGCAATGGGATCTGCTCATCCC 1533  
 1263 CAAGTCTTCTTAACTTCTGTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1322  
 1534 CAAGTCTTCTTAACTTCTGTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1593  
 1323 CTACCATCAGCTTACCTGAAAGAGCAGCGCGCCCTCAGCTGAAAGCGGAGTTGGAAA 1382  
 1594 CTACCATCAGCTTACCTGAAAGAGCAGCGCGCCCTCAGCTGAAAGCGGAGTTGGAAA 1653  
 1383 CTCATGCTGCTGACGGGCCACATCTTATCTGCTAGGGGGGATCTACCTCTGCTGGG 1442  
 1654 CTCATGCTGCTGACGGGCCACATCTTATCTGCTAGGGGGGATCTACCTCTGCTGGG 1713  
 1443 CCAGTCTGCTGATCTTGGGGCGCCAGCGTGTCTGATCTGATCTGATCTGATCTGATCT 1502  
 1714 CCAGTCTGCTGATCTTGGGGCGCCAGCGTGTCTGATCTGATCTGATCTGATCTGATCT 1773  
 1503 CTTTGAATCTCTTCTGTTTCCAGGCGCTGCTCAGAGTGTGTCCAGGTTGCTGTGTT 1562  
 1774 CTTTGAATCTCTTCTGTTTCCAGGCGCTGCTCAGAGTGTGTCCAGGTTGCTGTGTT 1833  
 1563 CTTGGCCATCGAGTGTGATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1622  
 1834 CTTGGCCATCGAGTGTGATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1893  
 1623 CTTGCTTACTATACAGTGTGCTTCCAGCACAGAGGATCTACAGTGTGATGATCCAGAA 1682  
 1894 CTTGCTTACTATACAGTGTGCTTCCAGCACAGAGGATCTACAGTGTGATGATCCAGAA 1953  
 1683 GGTCTATCTGCGGACCTGCTGCGCTTCTTCTGATCTGATCTGATCTGATCTGATCTG 1742  
 1954 GGTCTATCTGCGGACCTGCTGCGCTTCTTCTGATCTGATCTGATCTGATCTGATCTG 2013  
 1743 CGCTGTAGCCCTGTGTGAGCTGAGCCAGGAGGCTTGGCGCCCGCCGAAAGCTCTACAGGCC 1802  
 2014 CGCTGTAGCCCTGTGTGAGCTGAGCCAGGAGGCTTGGCGCCCGCCGAAAGCTCTACAGGCC 2073  
 1803 CAATGCCACAGATCAGTGTGAGCCCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1862  
 2074 CAATGCCACAGATCAGTGTGAGCCCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 2133  
 1863 GTACAGGGGTATCTTGAAGGCTCTCTGAGCTCTTCAAAATTCACCATCGGCATGGGCGA 1922

2134 GTACAGGGGTATCTCTGGAAGCCCTCTCTGGAGCTCTTCAAATTCACCATCGGCATGGCGA 2193  
 1923 GCTGCGCTTCCAGGAGCAGCTGACATTTCCGCGGCATGGTGTCTGCTGCTGCTGCTGCT 1982  
 2194 GCTGCGCTTCCAGGAGCAGCTGACATTTCCGCGGCATGGTGTCTGCTGCTGCTGCTGCT 2253  
 1983 COTGTGCTCACCTACATCTCTGCTCAACATGTCTCATGTCTCATGTCTCATGTCTCATGT 2042  
 2254 COTGTGCTCACCTACATCTCTGCTCAACATGTCTCATGTCTCATGTCTCATGTCTCATGT 2313  
 2043 CAACAGTGTGCGCATCTGACAGCTGAGCATCTGGAAGCTGCAAGAGCCATCTCTCTCTCT 2102  
 2314 CAACAGTGTGCGCATCTGACAGCTGGAAGCATCTGGAAGCTGCAAGAGCCATCTCTCTCTCT 2373  
 2103 GAGATGGAAGATGGCTATTGGTGTGAGGAAGAGCAGCGGGCAGGTGTGATGCTGAC 2162  
 2374 GAGATGGAAGATGGCTATTGGTGTGAGGAAGAGCAGCGGGCAGGTGTGATGCTGAC 2433  
 2163 COTGTGCACTAAGCCAGATGGCAGCCCGATGAGCGCTGGTGTCTTCAAGGTTGAGGAGGT 2222  
 2434 COTGTGCACTAAGCCAGATGGCAGCCCGATGAGCGCTGGTGTCTTCAAGGTTGAGGAGGT 2493  
 2223 GAATGGGCTTTCATGGGAGCAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2282  
 2494 GAATGGGCTTTCATGGGAGCAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2553  
 2283 TGTCCCTCGAACTCTCGAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2342  
 2554 TGTCCCTCGAACTCTCGAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2613  
 2343 TGTCCCTCGAGGAACTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2402  
 2614 TGTCCCTCGAGGAACTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2673  
 2403 CAGCAGAGGCGCAGAGGACAGAGCAGAGGATCTTTTCCAAACCATCTGCTGCTGCTGCTGCT 2462  
 2674 CAGCAGAGGCGCAGAGGACAGAGCAGAGGATCTTTTCCAAACCATCTGCTGCTGCTGCTGCT 2733  
 2463 TCCCACT 2469  
 2734 TCCCACT 2740

RESULT 6

ADP25060

ID ADP25060 standard; cDNA; 2807 BP.

XX ADP25060;

XX AC

XX ADP25060 (first entry)

XX 18-NOV-2004 (first entry)

XX PRO polypeptide encoding cDNA SEQ ID NO:2238.

DE

XX

XX

XX

XX

XX

XX

XX

XX

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XX

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XX

XX

XX

XX

ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;  
 immunosuppressive; osteopathic; antidiabetic; dermatological;  
 antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;  
 gene therapy; immune system.

Unidentified.

WO2004041170-A2.

21-MAY-2004.

30-OCT-2003; 2003WO-US034312.

01-NOV-2002; 2002US-0423394P.

(GETH ) GENENTECH INC.

Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WL;

Wu TD;

XX









Db 2358 CAAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCT 2417  
Qy 2103 GGAGATGGAGATGGCTATTGGTGTGTCAGGAAGACGCGGCGAGGTGTGATGCTGAC 2162  
Db 2418 GAGATGGAGATGGCTATTGGTGTGTCAGGAAGACGCGGCGAGGTGTGATGCTGAC 2477  
Qy 2163 CGTTGGCACTTAAGCCAGATGGCAGCCGGATGAGCGCTGTGCTTCAGGGGTGAGGAGGT 2222  
Db 2478 CGTTGGCACTTAAGCCAGATGGCAGCCGGATGAGCGCTGTGCTTCAGGGGTGAGGAGGT 2537  
Qy 2223 GAACCTGGCTTCATGGAGCAGACGCTGCTACGCTGTGTGAGGACCGGTTCAGGGGCAGG 2282  
Db 2538 GAACCTGGCTTCATGGAGCAGACGCTGCTACGCTGTGTGAGGACCGGTTCAGGGGCAGG 2597  
Qy 2283 TGTCCTCTGAACTCTCGAAGAACCTGTCTGGCTTCCCTCCCAAGAGGATGAGATGG 2342  
Db 2598 TGTCCTCTGAACTCTCGAAGAACCTGTCTGGCTTCCCTCCCAAGAGGATGAGATGG 2657  
Qy 2343 TGCTCTCGAGAAACCTATGTGCGCTGTCAGCTCTCCAGTCCAACTGATGGCCAGATG 2402  
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Qy 2403 CAGCAGAGGCCAGAGGACAGACAGAGGATCTTTTCCAAACCATCTGCTGTGCTGGGG 2462  
Db 2718 CAGCAGAGGCCAGAGGACAGACAGAGGATCTTTTCCAAACCATCTGCTGTGCTGGGG 2777  
Qy 2463 TCCAGT 2469  
Db 2778 TCCAGT 2784

RESULT 8  
ABL90839  
ID ABL90839 standard; cDNA; 2867 BP.  
XX ABL90839;  
AC  
XX  
DT 24-MAY-2002 (first entry)  
DE Human polynucleotide SEQ ID NO 1401.  
XX  
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein; gene; ss.  
XX Homo sapiens.  
OS  
XX WO200190304-A2.  
PN 29-NOV-2001.  
XX  
XX 18-MAY-2001; 2001WO-US016450.  
XX  
XX 19-MAY-2000; 2000US-0205515P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Birse CE, Rosen CA;  
XX WPI; 2002-122018/16.  
XX P-PSDB; ABB90430.  
XX  
XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and  
XX prevention of neural, immune system, muscular, reproductive,  
XX gastrointestinal, pulmonary, cardiovascular, renal and proliferative  
XX disorders.  
XX  
XX Claim 4; SEQ ID NO 1401; 2081pp + Sequence Listing; English.  
XX  
XX The invention relates to novel genes (ABL89449-ABL90853) and proteins  
XX (ABB89040-ABB90444) useful for preventing, treating or ameliorating

CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
CC ovarian cancer and other cancers of the adrenal gland, bone, marrow,  
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
CC infectious diseases such as viral, bacterial, fungal and parasitic  
CC infections. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 2867 BP; 589 A; 842 C; 826 G; 601 T; 0 U; 9 Other;  
  
Query Match 99.1%; Score 2447.4; DB 6; Length 2867;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2459; Conservative 3; Mismatches 4; Indels 1; Gaps 1;  
  
Qy 3 CGAGGCCGACGCGCAGCTGGGAGGAGACAGGACCCCTTGCATCTCCATCTGCACAGAGG 62  
Db 303 CAACACCGACGCGCAGCTGGGAGGAGACAGGACCCCTTGCATCTCCATCTGCACAGAGG 362  
  
Qy 63 TCCTGGCTGACCGAGCAGCTCTCTCTCTAGGATGACCTCACCTCCAGCTCTCCAGT 122  
Db 363 TCCTGGCTGACCGAGCAGCTCTCTCTCTAGGATGACCTCACCTCCAGCTCTCCAGT 422  
  
Qy 123 TTTTCAGTTGGAGACATTAGATGGAGGCCAAGAGATGGCTCTGAGCGGACAGAGAAA 182  
Db 423 TTTTCAGTTGGAGACATTAGATGGAGGCCAAGAGATGGCTCTGAGCGGACAGAGAAA 482  
  
Qy 183 GCTGGAATTTGGAGCGGGCTGCTCCATGGAGTACAGTTTCAGGGCCAGAGCCGAA 242  
Db 483 GCTGGAATTTGGAGCGGGCTGCTCCATGGAGTACAGTTTCAGGGCCAGAGCCGAA 542  
  
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Db 603 GGAATCCAAACCGATTTCACGAGATCGGTCTTTCAATGCGGTCTCCCGGGTGTCCCGGA 662  
  
Qy 363 GGAATCTGGTGGACTTTCAGAGTACCTGACAGACACAGCAAGTACTCTACCGACTCGGA 422  
Db 663 GGAATCTGGTGGACTTTCAGAGTACCTGACAGACACAGCAAGTACTCTACCGACTCGGA 722  
  
Qy 423 ATACACAGAGGGCTCCACAGGTAAGAGCTGCTGTAAGGCTGTGCTGAACCTTAAGGA 482  
Db 723 ATACACAGAGGGCTCCACAGGTAAGAGCTGCTGTAAGGCTGTGCTGAACCTTAAGGA 782  
  
Qy 483 CGGAGTCAATGCTGCAATTCGCACTGCTGAGATCGACAGGAGCTCTGGCAATCTCA 542  
Db 783 CGGAGTCAATGCTGCAATTCGCACTGCTGAGATCGACAGGAGCTCTGGCAATCTCA 842  
  
Qy 543 GCGCCTGGTAAATGCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTGTCACAT 602  
Db 843 GCGCCTGGTAAATGCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTGTCACAT 902  
  
Qy 603 CGCATTGAGAGAGGAGTCTGCAGTGTGTGAAGCTCTGTTGGAGATGGGGCCATGT 662  
Db 903 CGCATTGAGAGAGGAGTCTGCAGTGTGTGAAGCTCTGTTGGAGATGGGGCCATGT 962  
  
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Db 1644 CTCATGCTGCTGACGGGCCACATCCTTATCTCTGCTAGGGGGATCTACCTCTCGTGGG 1703  
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Db 1764 CTTTGAATCCTCTTCTGTTCAGGCCCTGTCTACAGTGTGTGTGTGTGTGTGT 1823  
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Db 1884 CTTGCTTTTACTATACAGT 1943  
QY 1683 GGTATCCTCGGGGACCTGT 1742  
Db 1944 GGTATCCTCGGGGACCTGT 2003  
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QY 1863 GTACAGGGGTATCTGTGAAGCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1922  
Db 2124 GTACAGGGGTATCTGTGAAGCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2183  
QY 1923 GCTGGCCCTCCAGAGCAGT 1982  
Db 2184 GCTGGCCCTCCAGAGCAGT 2243  
QY 1983 CGTGTGCTCACCTACATCTGT 2042  
Db 2244 CGTGTGCTCACCTACATCTGT 2303  
QY 2043 CAACAGTGTGCGCATGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2102  
Db 2304 CAACAGTGTGCGCATGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2363  
QY 2103 GGAGATGGAGATGGCTATTGT 2162  
Db 2364 GGAGATGGAGATGGCTATTGT 2423  
QY 2163 CGTTGGCACTAAGCCAGATGGCAGCCGGATGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 2222  
Db 2424 CGTTGGCACTAAGCCAGATGGCAGCCGGATGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 2483  
QY 2223 GAATGGGCTTCATGGAGCAGACGT 2282  
Db 2484 GAATGGGCTTCATGGAGCAGACGT 2543  
QY 2283 TGTCCCTCGAACTCTCGAGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2342  
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QY 2343 TGCCCTCTGAGGAAAATATGT 2402  
Db 2604 TGCCCTCTGAGGAAAATATGT 2663  
QY 2403 CAGCAGAGGCCAGAGCAGACAGCAGAGGATCTTTTCCAAACCATCTGTGTGTGTGTGTGTGT 2462  
Db 2664 CAGCAGAGGCCAGAGCAGACAGCAGAGGATCTTTTCCAAACCATCTGTGTGTGTGTGTGTGT 2723  
QY 2463 TCCAGT 2469  
|||||

Db 2724 TCCAGT 2730  
RESULT 10  
AA14874  
ID AAA14874 standard; DNA; 2765 BP.  
XX  
AC AAA14874;  
XX  
DT 08-AUG-2000 (first entry)  
XX  
DNA encoding a vanilloid receptor-like (VR-L) protein.  
XX  
Cation channel protein; vanilloid receptor-like 1 protein; VR-L;  
KW noxious heat; pain; inflammation; tissue damage; nociception;  
KW gene therapy; sensory neuron; immune system; analgesic; immunomodulatory;  
KW neuromodulatory; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 358..2652  
FT /tag= a  
FT /product= "vanilloid receptor-like (VR-L) protein"  
FT /transl\_except= (pos: 802..804, aa: Gly)  
FT /transl\_except= (pos: 955..957, aa: Lys)  
FT /transl\_except= (pos: 2035..2037, aa: Thr)  
FT /transl\_except= (pos: 2356..2358, aa: Xaa)  
FT /note= "Xaa is an unspecified amino acid"  
XX  
PN WO200022121-A2.  
XX  
PD 20-APR-2000.  
XX  
PF 08-OCT-1999; 99WO-GB003348.  
XX  
PR 09-OCT-1998; 98GB-00022124.  
XX  
PA (UNLO ) UNIV COLLEGE LONDON.  
XX  
PI Garcia R, Wood JN, England S;  
XX  
WI: 2000-317978/27.  
XX  
P-PSDB; AAY84834.  
PT Novel non-selective cation channel protein and nucleotides useful as  
PT screening agents and in gene therapy of disorders associated with sensory  
PT neurons and leucocytes such as pain, autoimmune disorders and leukemia.  
XX  
PS Claim 5; Fig 3A; 55pp; English.  
XX  
CC The present sequence encodes a non-selective cation channel protein,  
CC designated vanilloid receptor-like 1 (VR-L). The protein is obtained from  
CC human T lymphocytes. The VR-L protein is activated by noxious heat, and  
CC is not capsaicin sensitive. VR-L is expressed in sensory neurons, and is  
CC likely to play a role in mediating the pain and inflammation accompanying  
CC tissue damage (nociception). The VR-L polynucleotide is useful for  
CC influencing the electrophysiological and/or pharmacological properties of  
CC a cell, and is also useful in the gene therapy treatment of disorders  
CC associated with sensory neurons and/or cells of the immune system and  
CC also for the preparation of a medicament for use in gene therapy. The VR-  
CC L polynucleotides and polypeptides are useful for identifying a substance  
CC with ion-channel modulating activity (such as analgesics), or compounds  
CC which affect nociception, immunomodulatory agents, neuromodulatory agents  
XX  
SQ Sequence 2765 BP; 560 A; 821 C; 792 G; 589 T; 0 U; 3 Other;  
Query Match 98.4%; Score 2428.8; DB 3; Length 2765;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 2442; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 3 CGAGGCCGACGCGCAGCTGGGAGGAGACAGGACCCCTTCACATCTCCATCTGCACAGAGG 62  
|||||

Db 264 CAACACCGACGCGCAGCTGGAGGAAAGACAGGACCCTTGACATCTCCATCTGCACAGAGG 323  
Qy 63 TCCCTGGCTGACCGAGCAGCCTCCTCTCTAGATGACCTCACCTCCAGCTCTCCAGT 122  
Db 324 TCCCTGGCTGACCGAGCAGCCTCCTCTCTAGATGACCTCACCTCCAGCTCTCCAGT 383  
Qy 123 TTTTCAGGTTGGAGACATTAGATGGAGCCCAAGAGATGGCTCTGAGGCGGACAGAGGAAA 182  
Db 384 TTTTCAGGTTGGAGACATTAGATGGAGCCCAAGAGATGGCTCTGAGGCGGACAGAGGAAA 443  
Qy 183 GCTGGATTTGGAGCGGGCTGCTCTCCATGGAGTACAGTTCCAGGGCGAGACCGGAA 242  
Db 444 GCTGGATTTGGAGCGGGCTGCTCTCCATGGAGTACAGTTCCAGGGCGAGACCGGAA 503  
Qy 243 ATTGCGCCCTCAGATAGAGTCAACCTCAACTACCGAAAGGAAACAGGTCACAGTCAGCC 302  
Db 504 ATTGCGCCCTCAGATAGAGTCAACCTCAACTACCGAAAGGAAACAGGTCACAGTCAGCC 563  
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Db 564 GGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCGGA 623  
Qy 363 GGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACACAGCAAGTACTTCAACGACTCGGA 422  
Db 624 GGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACACAGCAAGTACTTCAACGACTCGGA 683  
Qy 423 ATACACAGAGGGCTCCACAGGTAAAGCTGCTGATGAAGGCTGTGCTGAACCTTAAGGA 482  
Db 684 ATACACAGAGGGCTCCACAGGTAAAGCTGCTGATGAAGGCTGTGCTGAACCTTAAGGA 743  
Qy 483 CGAGTCAATGCTGCAATTTGCCACCTGCTGCAGATCGACAGGACTCTTGGCAATCTCA 542  
Db 744 CGGGCTCAATGCTGCAATTTGCCACCTGCTGCAGATCGACAGGACTCTTGGCAATCTCA 803  
Qy 543 GCCCTCGTAAATGCCAGTGCAAGATGACTATTACCGAGGCGCACAGCGCTCTGCACAT 602  
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Qy 603 CGCCATTGAGAGAGGAGTCTGACGTGTGAGCTCTCTGGTGAGAAATGGGGCCAAATGT 662  
Db 864 CGCCATTGAGAGAGGAGTCTGACGTGTGAGCTCTCTGGTGAGAAATGGGGCCAAATGT 923  
Qy 663 GCATGCCCGGCGCTGCGGCGCTTCTTCCAGAGGGCCAAAGGACTTGTCTTTTATTTCCG 722  
Db 924 GCATGCCCGGCGCTGCGGCGCTTCTTCCAGAGTGGCCAAAGGACTTGTCTTTTATTTGG 983  
Qy 723 TGAGCTACCCCTCTCTTTTGGCGCTTGCAACAGCAGTGGATGTGTAAGCTACCTCCT 782  
Db 984 TGAGCTACCCCTCTCTTTTGGCGCTTGCAACAGCAGTGGATGTGTAAGCTACCTCCT 1043  
Qy 783 GGAGAACCCACACAGCCCGCAGCCTGCGAGGCCACTGACTCCCGAGGGCAACACAGTCTCT 842  
Db 1044 GGAGAACCCACACAGCCCGCAGCCTGCGAGGCCACTGACTCCCGAGGGCAACACAGTCTCT 1103  
Qy 843 GCATGCCCTAGTGATGATCTCGGACAACTCAGCTGAGAAATGTCATCTGTGACCCAGCAT 902  
Db 1104 GCATGCCCTAGTGATGATCTCGGACAACTCAGCTGAGAAATGTCATCTGTGACCCAGCAT 1163  
Qy 903 GTATGATGGGCTCTCCAAAGCTGGGGCCCGCTCTGCGCCTACCGTGAGCTTGAAGGACAT 962  
Db 1164 GTATGATGGGCTCTCCAAAGCTGGGGCCCGCTCTGCGCCTACCGTGAGCTTGAAGGACAT 1223  
Qy 963 CCGCAACCTTGAGATCTCAGCCTCTGAGAGCTGGCGCCGAGAGGGCGAAGATCGAGAT 1022  
Db 1224 CCGCAACCTTGAGATCTCAGCCTCTGAGAGCTGGCGCCGAGAGGGCGAAGATCGAGAT 1283  
Qy 1023 TTTTCAGGCACATCTGACGCGGAGTTTTCAGGACTGAGCCACCTTTCCCGAAAGTTTCA 1082  
Db 1284 TTTTCAGGCACATCTGACGCGGAGTTTTCAGGACTGAGCCACCTTTCCCGAAAGTTTCA 1343  
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Db 1344 CGAGTGGTGCTATGGGGCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGTGGACAGCTG 1403

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Qy 1203 AATGTCGTTTTGGAGCCCTGAAACAACTGCTGAGGCGGAAATGGGATCTGCTATCCC 1262  
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Qy 1563 CTTGGCCATCGAGTGTAACCTGCCCCTGCTGTGTGTCTGCGCTGGTGGCTGGCTGAA 1622  
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Qy 1623 CTTGCTTTACTATACAGTGGCTTCCAGCACACAGGCATCTACAGTGTCAATGATCCAGAA 1682  
Db 1884 CTTGCTTTACTATACAGTGGCTTCCAGCACACAGGCATCTACAGTGTCAATGATCCAGAA 1943  
Qy 1683 GGTTCATCTGCGGGAACCTGCTCGCTTCTTCTGATCTACTTACTTCTTCTTCTGCTT 1742  
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Qy 1743 CGCTGTAGCCCTGCTGAGCTGAGCCAGGAGCTTGGCGCCCGCAAGCTCTTACAGGCC 1802  
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Db 2064 CAATGCCACAGATCAGTGCAGCCCATGGAGGACAGGAGGACAGGGGCAACCGGGCCCA 2123  
Qy 1863 GTACAGGGGTATCTTGAAGCCCTCTTGGAGCTCTTCAAAATTCACATCGGCATGGCGGA 1922  
Db 2124 GTACAGGGGTATCTTGAAGCCCTCTTGGAGCTCTTGGAGCTCTTCAAAATTCACATCGGCATGGCGGA 2183  
Qy 1923 GCTGGCCTTCCAGGAGCAGTGCATTTCCGCGCAGCTGGTGTGCTGTGCTGTGGCCTA 1982  
Db 2184 GCTGGCCTTCCAGGAGCAGTGCATTTCCGCGCAGCTGGTGTGCTGTGCTGTGGCCTA 2243  
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Qy 2103 GGAGATGGAGAAATGGCTATTGGTGTGAGGAAAGACAGCGGGCAGGTGTGATGTGAC 2162  
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QY	661	GTGCATGCGCGGCTGCGCGCTCTTCCAGAGGCGCCAGGACTTGTCTTTATTTC	720	QY	1741	TTTCGTGTAGCCCTGTGTAGCCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCTCTACAGGC	1800
DB	947	GTGCATGCGCGGCGCTGCGCGCTCTTCCAGAGGCGCCAGGACTTGTCTTTATTTC	1006	DB	2024	TTTCGTGTAGCCCTGTGTAGCCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCTCTACAGGC	2083
QY	721	GGTGAGCTACCCCTCTCTTTGGCGGCTTGACCAAGCAGTGGGATGTGGTAACTACCTC	780	QY	1801	CCCAATGCCACAGAGTCAGTCAGCCCATGGAGGACAGGAGGACAGGACGAGGACGCGGCC	1860
DB	1007	GGTGAGCTACCCCTCTCTTTGGCGGCTTGACCAAGCAGTGGGATGTGGTAACTACCTC	1066	DB	2084	CCCAATGCCACAGAGTCAGTCAGCCCATGGAGGACAGGAGGACAGGACGAGGACGCGGCC	2143
QY	781	CTGGAGAACCCACACAGAGCCCGCAGCTGCGAGGCCATCTGATCTCCAGGCGCAACAGTC	840	QY	1861	CAGTACAGGGGTATCCTGGAAGCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGGC	1920
DB	1067	CTGGAGAACCCACACAGAGCCCGCAGCTGCGAGGCCATCTGATCTCCAGGCGCAACAGTC	1126	DB	2144	CAGTACAGGGGTATCCTGGAAGCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGGC	2203
QY	841	CTGCATGCCCTAGTGATCTCGGACAACTCAGCTGAGAACATTCGACTGGTGACGAGC	900	QY	1921	GAGCTGGCTTCCAGAGCAGTCGACTTTCGCGGCGCATGGTGTCTGTCTGTCTGTGGCC	1980
DB	1127	CTGCATGCCCTAGTGATCTCGGACAACTCAGCTGAGAACATTCGACTGGTGACGAGC	1186	DB	2204	GAGCTGGCTTCCAGAGCAGTCGACTTTCGCGGCGCATGGTGTCTGTCTGTCTGTGGCC	2263
QY	901	ATGTATGATGGGCTCTCTCAAGCTGGGGCCCGCTCTGCGCTACCGTGCAGCTTGGAGC	960	QY	1981	TAGTGTCTCTCACCTACATCTGCTGCTCAATGCTCATCGCCCTCATGAGCGAGACC	2040
DB	1187	ATGTATGATGGGCTCTCTCAAGCTGGGGCCCGCTCTGCGCTACCGTGCAGCTTGGAGC	1246	DB	2264	TAGTGTCTCTCACCTACATCTGCTGCTCAATGCTCATCGCCCTCATGAGCGAGACC	2323
QY	961	ATCCGAACTGTCAGGATCTCAAGCTCTGAAGCTGGCCCGCCCAAGAGGCGCAAGATCGAG	1020	QY	2041	GTCAACAGTGTGCGCACTGACAGCTGAGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTC	2100
DB	1247	ATCCGAACTGTCAGGATCTCAAGCTCTGAAGCTGGCCCGCCCAAGAGGCGCAAGATCGAG	1306	DB	2324	GTCAACAGTGTGCGCACTGACAGCTGAGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTC	2383
QY	1021	ATTTTCAGGCACATCTGACAGCGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTTC	1080	QY	2101	CTGGAGATGGAGAAATGGCTATTGGTGTGAGGAAAGAGCAGCGGCGAGGTGTGATGCTG	2160
DB	1307	ATTTTCAGGCACATCTGACAGCGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTTC	1366	DB	2384	CTGGAGATGGAGAAATGGCTATTGGTGTGAGGAAAGAGCAGCGGCGAGGTGTGATGCTG	2443
QY	1081	ACCGAGTGTGTATGCGCTGTCGCGGCTGTGCTGTATGACCTGGCTTCTGTGGACAGC	1140	QY	2161	ACCGTTGGCACAATGAGCCAGATGGCAGCCCGGATGAGCGCTGTGCTTTCAGGGTGGAGGAG	2220
DB	1367	ACCGAGTGTGTATGCGCTGTCGCGGCTGTGCTGTATGACCTGGCTTCTGTGGACAGC	1426	DB	2444	ACCGTTGGCACAATGAGCCAGATGGCAGCCCGGATGAGCGCTGTGCTTTCAGGGTGGAGGAG	2503
QY	1141	TGTGAGGAGAACTCAGTGTGAGATCAATGGCTTTTCAATGTCAGAGCCCGGACCGAGAC	1200	QY	2221	GTGAACCTGGGCTTTCATGGAGCAGACGCTGCGCTTACGCTGTGTGAGGACCCGTCAGGGGCA	2280
DB	1427	TGTGAGGAGAACTCAGTGTGAGATCAATGGCTTTTCAATGTCAGAGCCCGGACCGAGAC	1486	DB	2504	GTGAACCTGGGCTTTCATGGAGCAGACGCTGCGCTTACGCTGTGTGAGGACCCGTCAGGGGCA	2563
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DB	1487	CGAATGCTGTTTGGAGCCCTGACAACTGCTGAGCGGAAATGGGATCTGCTCATC	1546	DB	2564	GGTGTCCCTCGAACTCTCGAGAAACCTGTCTGGCTTCCCTTCCCAAGGAGGATGAGAT	2623
QY	1261	CCCAAGTCTTCTTAAATCTCTGTGTAATCTGATCTACATGTTTCATCTTTCACCGCTGTT	1320	QY	2341	GGTGTCCCTCGAGAAATCTATGTGCGCGCTCCAGCTCTCCAGTCCCACTCATGAGCCGAG	2400
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QY	1321	GCCTACCATCAGCCTACCTGGAAGAGCAGCGCCCTCACTGAAAGCGGAGTTGGA	1380	QY	2401	TGCAGCAGAGGCGCCAGAGGACAGAGGATCTTTCACCAACCACTCTGCTGGCTCTGG	2460
DB	1607	GCCTACCATCAGCCTACCTGGAAGAGCAGCGCCCTCACTGAAAGCGGAGTTGGA	1663	DB	2684	TGCAGCAGAGGCGCCAGAGGACAGAGGATCTTTCACCAACCACTCTGCTGGCTCTGG	2743
QY	1381	AATCCATGCTGTGACGGGCGACATCTTATCTGCTAGGGGGATCTACCTCTCGTG	1440	QY	2461	GGTCCCAGT 2469	
DB	1664	AATCCATGCTGTGACGGGCGACATCTTATCTGCTAGGGGGATCTACCTCTCGTG	1723	DB	2744	GGTCCCAGT 2752	
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QY	1501	TACTTTGAAATCCCTCTTCTGTTCCAGGCCCTGCTCAAGTGGTGTCCAGGTTGCTGTGT	1560	ACD91294			
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QY	1561	TTCTGGCCATCGAGTGTACTGCGCTGCTGTGTGTGCTGCTGGCTGGCTGGCTG	1620	XX	ACD91294;		
DB	1844	TTCTGGCCATCGAGTGTGTACTGCGCTGCTGTGTGTGCTGCTGGCTGGCTGGCTG	1903	XX	22-SEP-2003 (first entry)		
QY	1621	AACCTGCTTTACTATACAGTGGCTTCCAGCACACAGGCACTACAGTGTATCATCATCAG	1680	XX	Human vanilloid receptor-2 cdna.		
DB	1904	AACCTGCTTTACTATACAGTGGCTTCCAGCACACAGGCACTACAGTGTATCATCATCAG	1963	XX	Human; ss; gene therapy; multiple sclerosis; chromosome identification;		
QY	1681	AAGGTCACTCTCGCGGACCTGCTGGCTTCTCTGATCTACTTACTTACTTCTCTTTCGGC	1740	XX	vanilloid receptor-2; chronic pain syndrome; host defence dysfunction;		
DB	1964	AAGGTCACTCTCGCGGACCTGCTGGCTTCTCTGATCTACTTACTTACTTCTCTTTCGGC	2023	XX	congenital pain insensitivity; arthritis; neurodegenerative disorder;		
				XX	immune surveillance dysfunction; systemic lupus erythematosus; stroke;		
				XX	inflammation; ischaemia; myocardial infarction; Alzheimer's disease;		
				XX	Parkinson's disease; infection; viral infection; autoimmune disease;		
				XX	septic shock; liver disease; cachexia; anorexia; immune dysfunction;		
				XX	allergy; gene mapping; AIDS; gene.		
				OS	Homo sapiens.		

XX US2003022289-A1.  
PN 30-JAN-2003.  
XX  
XX 03-MAY-2002; 2002US-00137316.  
PF  
XX 11-AUG-1998; 98US-00132316.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Young PE, Ruben SM;  
PI  
XX WPI; 2003-540138/51.  
DR P-PSDB; ABO42807.  
XX  
XX New nucleic acid molecule encoding vanilloid receptor 2 polypeptides,  
PT useful for drug screening and for diagnosing, preventing or treating  
PT disorders such as chronic pain syndromes, inflammation, ischemia or  
PT autoimmune diseases.  
XX  
XX Claim 4; Fig 1; 82pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule encoding a  
CC vanilloid receptor-2 polypeptide. The composition and methods are useful  
CC for drug screening and for diagnosing, preventing or treating disorders  
CC such as chronic pain syndromes, congenital pain insensitivity, arthritis,  
CC inflammation, ischaemia (e.g. stroke or myocardial infarction), host  
CC defence dysfunction, immune surveillance dysfunction, neurodegenerative  
CC disorders (e.g. Alzheimer's disease or Parkinson's disease), multiple  
CC sclerosis, infections (e.g. viral including AIDS), autoimmunity (e.g.  
CC systemic lupus erythematosus), septic shock, liver disease, cachexia,  
CC anorexia, immune dysfunction or allergy. The nucleic acid may also be  
CC used for gene mapping or chromosome identification. The present sequence  
CC represents cDNA encoding the human vanilloid receptor-2  
XX  
XX Sequence 2805 BP; 579 A; 830 C; 803 G; 593 T; 0 U; 0 Other;  
SQ

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287 CAACACCGACCGCCACGTGGGAGGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG 346  
63 TCCTGGCTGGACCGGAGC--AGCCTCTCTCTCTAGGATGACCTCACCCCTCCAGCTCTCCA 120  
347 TCCTGGCTGGACCGGAGTATGCTCTCTCTCTAGGATGACCTCACCCCTCCAGCTCTCCA 406  
121 GTTTTCAGGTTGGAGACATTAGATGGAGGCGCAAGAGATGGCTCTGAGGCGGACAGAGGA 180  
407 GTTTTCAGGTTGGAGACATTAGATGGAGGCGCAAGAGATGGCTCTGAGGCGGACAGAGGA 466  
181 AAGCTGGATTTTGGAGCGGGCTCCCTCCATGGAGTCACAGTTCCAGGCGGAGACCGG 240  
467 AAGCTGGATTTTGGAGCGGGCTCCCTCCATGGAGTCACAGTTCCAGGCGGAGACCGG 526  
241 AAATTGCGCCCTCAGATAAGAGTCAACTCACTACCGAAAGGGAACAGGTGGCCAGTTCAG 300  
527 AAATTGCGCCCTCAGATAAGAGTCAACTCACTACCGAAAGGGAACAGGTGGCCAGTTCAG 586  
301 CCGGATCCAAACCGAATTGACCGAGATCGGCTCTTCAATCGGTCTTCCCGGGGTGTCGCC 360  
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361 GAGGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACAGGATACCTCAACCGACTCG 420  
647 GAGGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACAGGATACCTCAACCGACTCG 706  
421 GAATACACAGAGGGCTCCACAGGTAAAGACGTGCTGATGAAGGTGTGCTGGAACCTTAAG 480  
707 GAATACACAGAGGGCTCCACAGGTAAAGACGTGCTGATGAAGGTGTGCTGGAACCTTAAG 766

QY 481 GACGGAGTCAATGCTTGCATTTCTGCCACTGTCTGCAGATCGACAGGGACTCTGGCAATCCT 540  
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QY 541 CAGCCCTCGTAAATGCCAGTGCACAGATGACTATTACCAGAGGCCACAGCGCTCTGCAC 600  
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Qy	1819	GTGCAGCCCATGGAGGACAGGAGGACAGGGGCAACGGGGCCCATGATACAGGGGTATCCCTG	1878
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Qy	2059	GACAGCTGGAGCATCTGGAAGCTCGAAGAGCCATCTGTCTCTGGAGATGGAGATGGC	2118
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Db	2221	GAGAACCTCTCTCGGTTCCCTCCCAAGGAGGATGAGGATGGTCTCTGAGGAAAC	2288
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AC	AAZ07114;		
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DT	08-OCT-1999 (first entry)		
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DE	Human vanilloid receptor homologue VANILREP2 encoding cDNA.		
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KW	Human; vanilloid receptor homologue; VANILREP2; polymorphic variant;		
KW	PVP-1; therapy; diagnosis; chronic pain; neuropathic; postoperative;		
KW	rheumatoid arthritis; neuralgia; algesia; nerve injury; ischaemia;		
KW	neurodegeneration; stroke; incontinence; inflammatory disorder; SS.		
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OS	Homo sapiens.		
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FT		/note= "vanilloid receptor homologue"	
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PD	29-JUL-1999.		
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PF	25-JAN-1999; 99WO-EP000420.		
XX			
PR	27-JAN-1998; 98EP-00300549.		
PR	26-OCT-1998; 98GB-00023421.		
PR	20-JAN-1999; 99GB-00001209.		
XX			
PA	(SMIK ) SMITHKLINE BEECHAM PLC.		
XX			
PI	Davis JB, Duckworth DM, Hayes PD;		
XX			
DR	WPI; 1999-479049/40.		
DR	P-PSDB; AAY29469.		
PT	New human vanilloid receptor homologues (VANILREP2).		
XX			
PS	Claim 9; Page 29-30; 47pp; English.		
XX			
CC	The present sequence encodes a human vanilloid receptor homologue,		
CC	designated VANILREP2. VANILREP2 can be used to diagnose disease or		
CC	susceptibility to disease related to expression or activity of VANILREP2		
CC	polypeptides. VANILREP2 may be used to treat diseases including pain,		
CC	(for example chronic, neuropathic, postoperative, rheumatoid arthritis,		
CC	neuralgia, algesia, nerve injury, ischaemia, neurodegeneration, stroke,		
CC	incontinence, and inflammatory disorders		
XX			
SQ	Sequence 2351 BP; 486 A; 684 C; 676 G; 505 T; 0 U; 0 Other;		
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Best Local Similarity 95.1%; Score 2347.8; DB 2; Length 2351;			
Matches 2349; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
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Db	2281	GCTCCTCCAGTCCCAACTGATGGCCCAAGATGCACGAGGAGGCCACAGAGGACAGAGCAGAGGA	2340
Qy	2433	TCTTTCCACC	2443
Db	2341	TCTTTCCACC	2351

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Job time : 1233 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:02:42 ; Search time 10359 Seconds  
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- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2459	99.6	2780	9	BC051305 Homo sapi
4	2455.8	99.5	2825	6	AX179742 Sequence 1
5	2444.6	99.0	2783	6	A94121 Sequence 1
6	2444.6	99.0	2783	6	AX017826 Sequence 1
7	2428.8	98.4	2765	6	BD251411 Ion chann
8	2428.8	98.4	2765	6	AX023769 Sequence
9	2424.6	98.2	2805	6	AX225700 Sequence
10	2397.8	97.1	2507	9	AF103906 Homo sapi
11	2379.4	96.4	2397	9	AF129112 Homo sapi
12	2378.4	96.3	2380	6	AX181402 Sequence
13	2378.4	96.3	2380	6	BD131756 Nucleic a
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15	2347.8	95.1	2351	6	BD130940 Human van
16	2347.8	95.1	2351	9	AJ487963 Homo sapi
17	2333.4	94.5	2348	6	AX019710 Sequence
18	2333.4	94.5	2348	6	BD130942 Human van
19	2292	92.8	2292	6	BD264280 Novel mem

20	2259.2	91.5	2779	6	BD191226	BD191226 186 human
21	2259.2	91.5	2779	6	AX924736	AX924736 Sequence
22	2061.8	83.5	2860	6	BD191342	BD191342 186 human
23	2061.8	83.5	2860	6	AX924852	AX924852 Sequence
24	1720	69.7	1790	6	AR220826	AR220826 Sequence
25	1581.2	64.0	2710	10	BC005415	BC005415 Mus muscu
26	1572	63.7	2824	10	AB021665	AB021665 Mus muscu
27	1571.2	63.6	2419	10	AY487844	AY487844 F-11 rat/
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ALIGNMENTS

BD264279 2809 bp DNA linear PAT 17-JUL-2003  
Novel members of protein capsaicin/vanilloid receptor family and  
utilization thereof.  
BD264279 GI:33074047  
VERSION JP 2002531069-A/3.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 2809)  
AUTHORS Curtis,R.A.J.  
TITLE Novel members of protein capsaicin/vanilloid receptor family and  
utilization thereof  
JOURNAL Patent: JP 2002531069-A 3 24-SEP-2002;  
MILLENNIUM PHARMACEUTICALS INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002531069-A/3  
PD 24-SEP-2002  
PF 12-NOV-1999 JP 2000582560  
PR 13-NOV-1998 US 60/108322,28-DEC-1998 US 60/114078 PR  
26-FEB-1999 US 09/258633,19-OCT-1999 US 09/421134 PI RORY A  
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PC C12N15/09,A61K45/00,A61P25/04,C07K14/705,C07K16/28,C07K19/00,  
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PC C12N1/15,G01N33/50,  
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PC G01N33/53,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC Novel  
members of protein capsaicin/vanilloid receptor family CC  
and  
CC utilization thereof  
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 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2780)  
 Srausberg R.L., Reingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,  
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 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
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 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
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 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullighy, S.J., Bosak, S.A., McSwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
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 Generation and initial analysis of more than 15,000 full-length  
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 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL 12477932  
 PUBMED 2 (bases 1 to 2780)  
 REFERENCE Strausberg, R.  
 AUTHORS Direct Submission  
 TITLE Submitted (25-APR-2003) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC/DCTP  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
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 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lari, P., Legaspi, R.,  
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 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
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 Db 2482 GAACTGGGCTTCAATGGGAGCAGACGCTGCTTACGCTGTGTGAGGACCCGTCAGGGGGCAGG 2541  
 |||||  
 QY 2283 TGTCTCTCGAACTCTCGAAGAACCTGTCTCTGGCTTCCCTTCCCAAGAGGATGAGGATGG 2342  
 |||||  
 Db 2542 TGTCTCTCGAACTCTCGAAGAACCTGTCTCTGGCTTCCCTTCCCAAGAGGATGAGGATGG 2601  
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 QY 2343 TGCCTCTGAGGAAAACTATGTGCCCTCCAGCTCTCCAGTCCAACTGATGGGCCAGATG 2402  
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 Db 2602 TGCCTCTGAGGAAAACTATGTGCCCTCCAGCTCTCCAGTCCAACTGATGGGCCAGATG 2661  
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 QY 2403 CAGCAGAGGCCAGAGGACAGAGCAGGAGTCTTTTCCAAACCATCTGCTGGCTCTGGGG 2462  
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Db      2662  CAGCAGGAGCCAGAGGACAGACAGAGGATCTTTCCAAACCATCTGCTGGCTCTGGGG 2721
Qy      2463  TCCAGT 2469
Db      2722  TCCAGT 2728
|||
|||
|||

RESULT 4
LOCUS   AX179742                2825 bp      DNA      linear      PAT 06-AUG-2001
DEFINITION Sequence 30 from Patent WO0146258.
ACCESSION AX179742
VERSION   AX179742.1 GI:15132106
KEYWORDS  Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS  Baughn, M.R., Burford, N., Au-Young, J., Lu, D.A., Yang, J., Reddy, R.,
          Lal, P., Hillman, J.L., Azimzai, Y., Yue, H., Nguyen, D.B., Yao, M.G.,
          Gandhi, A.R., Tang, Y.T. and Khan, F.A.
          Transпорters and ion channels
          Patent: WO 0146258-A 30 28-JUN-2001;
          Incyte Genomics, Inc. (US)
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      3  CGAGCCGACGCGCAGCTGGGAGAGACAGGACCCCTTGACNTCTCCATCTGCACAGAGG 62
Db      318  CAACACCGACGCGCAGCTGGGAGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG 377

Qy      63  TCCTGGCTGGACCCAGCAGCCTCTCTCTCTAGATGACCTCAACCTCCAGCTCTCCAGT 122
Db      378  TCCTGGCTGGACCGAGCAGCTCTCTCTCTAGATGACCTCAACCTCCAGCTCTCCAGT 437

Qy      123  TTTCCAGGTTGGAGACATTAGATGAGGCCAAGAGATGGCTCTGAGCGGCACAGAGAAA 182
Db      438  TTTCCAGGTTGGAGACATTAGATGAGGCCAAGAGATGGCTCTGAGCGGCACAGAGAAA 497

Qy      183  GCTGGATTTGGGAGCGGGCTGCCCTCCATGGAGTCAAGTTCCAGGGCGAGGACCGGAA 242
Db      498  GCTGGATTTGGGAGCGGGCTGCCCTCCATGGAGTCAAGTTCCAGGGCGAGGACCGGAA 557

Qy      243  ATTCGCCCTCAGATAAGAGTCAACCTCACTACCGAAAGGAAACAGGTGCCAGTCAAGCC 302
Db      558  ATTCGCCCTCAGATAAGAGTCAACCTCACTACCGAAAGGAAACAGGTGCCAGTCAAGCC 617

Qy      303  GGATCCAAACCGATTGACCGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTGTCGCCGA 362
Db      618  GGATCCAAACCGATTGACCGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTGTCGCCGA 677

Qy      363  GGATCTGGCTGGACTTCAGAGTACCTGAGCAAGACCGAAGTACCTCAACCGACTCGGA 422
Db      678  GGATCTGGCTGGACTTCAGAGTACCTGAGCAAGACCGAAGTACCTCAACCGACTCGGA 737

Qy      423  ATACACAGAGGCTCCACAGGTAAAGCTGCTGATGAAGCTGTGCTGAACCTTAAAGGA 482
Db      738  ATACACAGAGGCTCCACAGGTAAAGCTGCTGATGAAGCTGTGCTGAACCTTAAAGGA 797

Qy      483  CGGAGTCAATGCTGCAATTTGCCACTGCTGCAAGATCGACAGGAGCTCTGGCAATCTCTCA 542
Db      798  CGGAGTCAATGCTGCAATTTGCCACTGCTGCAAGATCGACAGGAGCTCTGGCAATCTCTCA 857

543  GCCCTCTGTAAATGCCAGTGCACAGATGACTATTACCGAGCCACAGCGCTCTGCACAT 602
858  GCCCTCTGTAAATGCCAGTGCACAGATGACTATTACCGAGCCACAGCGCTCTGCACAT 917
603  CGCCATTGAGAAAGAGAGTCTGCAGTGTGTGAAGTCTCTGGTGGAGAAATGGGGCCCAATGT 662
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963  CGCAACCTTGAGGATCTCAAGCTCTGAGCTGGCGGCGGCTGAGGACATCTCCAGAAAGTTCAC 1082
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1578  CAAGTTCTTCTTAAACTTCTCTGTAAATCTGATCTACATGTTCACTTCAACGCTGTTC 1637
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1638  CTACCATCAGCTTACCTTGAAGAGAGGCGGCGGCTTCACTGAAAGCGGAGGTGGAAA 1697
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1878  CCTGGCCATCGAGTGGTACCTGCGGCTGTTGTCTGCGCTGGTGTCTGGCTGCTGCTGAA 1937
1623  CCTGCTTTACTATACAGCTGGCTTCCAGCACACAGGCACTTACAGTGTCTATGATCCAGAA 1982
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Db	1938	CTGCTTTACTATACAGTGGCTTCCAGCACACAGGATCTACAGTGTGATGATCCAGAA	1997
Qy	1683	GGTCATCTCGGGACCTGCTGGCTTCTTCTGATCTACTTGTCTTCTTTCGGCTT	1742
Db	1998	GGTCATCTCGGGACCTGCTGGCTTCTTCTGATCTACTTGTCTTCTTTCGGCTT	2057
Qy	1743	CGCTGTAGCCCTGGTGTAGCCCTGAGCCGACGAGGCTTGGCGGCCCGAAGCTCTCTACAGGCC	1802
Db	2058	CGCTGTAGCCCTGGTGTAGCCCTGAGCCGAGGAGGCTTGGCGGCCCGAAGCTCTCTACAGGCC	2117
Qy	1803	CAATGCCACAGAGTCACTGTGAGCCCTGAGGAGGACAGGAGGACAGGGCAACGGGCCCCA	1862
Db	2118	CAATGCCACAGAGTCACTGTGAGCCCTGAGGAGGACAGGAGGACAGGGCAACGGGCCCCA	2177
Qy	1863	GTACAGGGGTATCTTGGAGCCCTCTTGGAGCTCTTCAATTCACCATGGCATGGCGCA	1922
Db	2178	GTACAGGGGTATCTTGGAGCCCTCTTGGAGCTCTTCAATTCACCATGGCATGGCGCA	2237
Qy	1923	GCTGGCCTTCAGAGCAGCTGCACTTCCCGGCGATGGTCTGCTGCTGCTGCGCTTA	1982
Db	2238	GCTGGCCTTCAGAGCAGCTGCACTTCCCGGCGATGGTCTGCTGCTGCTGCGCTTA	2297
Qy	1983	CGTGTCTCACTACATCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACCGT	2042
Db	2298	CGTGTCTCACTACATCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACCGT	2357
Qy	2043	CAACAGTGTCCGCACTGACAGCTGGAGCATCTGGAGCTGACAGAAAGCCATCTCTGTCT	2102
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Qy	2103	GGAGATGGAGAAATGCTATTGGTGGTGCAGGAGAGACAGCGGCGAGGTGTGATGCTGAC	2162
Db	2418	GGAGATGGAGAAATGCTATTGGTGGTGCAGGAGAGACAGCGGCGAGGTGTGATGCTGAC	2477
Qy	2163	CGTTGGCAGTAAGCCAGATCGCAGCCGATGAGCGTGTGCTTCAAGGCTGAGGAGGT	2222
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Qy	2223	GAACCTGGCTTCAATGGGAGCAGACGCTGCTCACTGCTGTGTGAGGACCCGTCAGGGGCGAG	2282
Db	2538	GAACCTGGCTTCAATGGGAGCAGACGCTGCTCACTGCTGTGTGAGGACCCGTCAGGGGCGAG	2597
Qy	2283	TGTCCTCTGAACTCTCGAGAACCTGTCTGGCTTCCCTCCCAAGAGGATGAGATGG	2342
Db	2598	TGTCCTCTGAACTCTCGAGAACCTGTCTGGCTTCCCTCCCAAGAGGATGAGATGG	2657
Qy	2343	TGCTCTTGAGAAACTATGTGCGCGTCCAGCTCCTCCAGTCCAACTGATGGGCCAGATG	2402
Db	2658	TGCTCTTGAGAAACTATGTGCGCGTCCAGCTCCTCCAGTCCAACTGATGGGCCAGATG	2717
Qy	2403	CAGCAGGAGCCAGAGGACAGAGCAGAGGATCTTTTCAACCAATCTGTGCTGTGGG	2462
Db	2718	CAGCAGGAGCCAGAGGACAGAGCAGAGGATCTTTTCAACCAATCTGTGCTGTGGG	2777
Qy	2463	TCCAGT 2469	
Db	2778	TCCAGT 2784	
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LOCUS	A94121	2783 bp	DNA
DEFINITION	Sequence 1 from Patent EP0953638.		circular PAT 26-JAN-2000
ACCESSION	A94121		
VERSION	A94121.1	GI:6778849	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 2783)		
AUTHORS	Renard, S. and Partiseti, M.		

TITLE	Human vanilloid receptor-like cation channel		
JOURNAL	Patent: EP 0953638-A 1 03-NOV-1999;		
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ORIGIN			
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Best Local Similarity	99.7%; Pred. No. 0;		
Matches 2460; Conservative	0; Mismatches 4; Indels 3; Gaps 1;		
QY	3	CGAGGCCGACGCGCAGCTGGGAGGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG	62
Db	267	CAACACCGACGCGCAGCTGGGAGGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG	326
QY	63	TCCTGGCTGGACCGGACGAGCTCCTCTCTTAGGATGACCTCAACCTCCAGCTCTCCAGT	122
Db	327	TCCTGGCTGGACCGGACGAGCTCCTCTCTTAGGATGACCTCAACCTCCAGCTCTCCAGT	386
QY	123	TTTCAGGTTGGAGACATTAGATGGAGGCCAAGAAGATGGCTCTTGAGGCGGACAGAGGAAA	182
Db	387	TTTCAGGTTGGAGACATTAGATGGAGGCCAAGAAGATGGCTCTTGAGGCGGACAGAGGAAA	446
QY	183	GCTGATATTTGGGAGCGGGCTGCTCCCATGGAGTACAGTTCCAGGGCGGAGACCGGAA	242
Db	447	GCTGATATTTGGGAGCGGGCTGCTCCCATGGAGTACAGTTCCAGGGCGGAGACCGGAA	506
QY	243	ATTTCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAGGGAACAGGTGCCAGTCAGCC	302
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QY	303	GGATCCAAACCGATTGACCGGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCCGA	362
Db	567	GGATCCAAACCGATTGACCGGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCCGA	626
QY	363	GGATCTGGCTGACTTCCAGAGTACTGTGACGACGACCGACAGTACTCTACCGACTCGGA	422
Db	627	GGATCTGGCTGACTTCCAGAGTACTGTGACGACGACCGACAGTACTCTACCGACTCGGA	686
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KEYWORDS	Homo sapiens (human)	QY	783	GGAGAACCCACACACCGCCGCGCAGCTGCAGGCCACTGACTCCAGGGCAACACAGCTCCT	842
SOURCE	Homo sapiens	Db	1047	GGAGAACCCACACACCGCCGCGCAGCTGCAGGCCACTGACTCCAGGGCAACACAGCTCCT	1106
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	QY	843	GCATGCCCTAGTGATGATCTCGGACAACTCAGCTGAGAACATTGACCTGGTACACAGCAT	902
REFERENCE	1. Renard, S. and Partiseti, M.	Db	1107	GCATGCCCTAGTGATGATCTCGGACAACTCAGCTGAGAACATTGACCTGGTACACAGCAT	1166
AUTHORS	A human vanilloid receptor-like cation channel	QY	903	GTATGATGGGCTCTCCAAAGCTGGGGCCGCTCTGCTCCCTACCTGTCAGCTGAGAGCAT	962
TITLE	Patent: WO 9946377-A 1 16-SEP-1999;	Db	1167	GTATGATGGGCTCTCCAAAGCTGGGGCCGCTCTGCTCCCTACCTGTCAGCTGAGAGCAT	1226
JOURNAL	SANOPI SYNTHELABO (FR); RENARD STEPHANE (FR); PARTISETI MICHEL (FR)	QY	963	CGGCAACCTGCAGGATCTCAGCCCTCTGAAGCTGCGCCGCAAGGAGGGCAAGATCCAGAT	1022
FEATURES	Location/Qualifiers	Db	1227	CGGCAACCTGCAGGATCTCAGCCCTCTGAAGCTGCGCCGCAAGGAGGGCAAGATCCAGAT	1286
source	1..2783	QY	1023	TTTTCAGGCACATCTCTGCAGCGGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTAC	1082
ORIGIN	Query Match 99.0%; Score 2444.6; DB 6; Length 2783; Best Local Similarity 99.7%; Pred. No. 0; Matches 2460; Conservative 0; Mismatches 4; Indels 3; Gaps 1;	Db	1287	TTTTCAGGCACATCTCTGCAGCGGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTAC	1346
		QY	1083	CGAGTGGTGTCTATGGGCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGTGACAGCTG	1142
		Db	1347	CGAGTGGTGTCTATGGGCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGTGACAGCTG	1406
		QY	1143	TCGAGAGAACTCAGTGTGGAGATCATTCGCCCTTTCATTGCAAGAGCCGACACGACCG	1202
		Db	1407	TCGAGAGAACTCAGTGTGGAGATCATTCGCCCTTTCATTGCAAGAGCCGACACGACCG	1466
		QY	1203	AATGSGTCTGTTTGGAGCCCTCGAAACAACTGCTGCAGGCGAAATGGGATCTGCTCATCC	1262
		Db	1467	AATGSGTCTGTTTGGAGCCCTCGAAACAACTGCTGCAGGCGAAATGGGATCTGCTCATCC	1526
		QY	1263	CAAGTCTCTTAAACTCTGTGTAACTGATCTACATGTTCACTTCACGCTGTGTC	1322
		Db	1527	CAAGTCTCTTAAACTCTGTGTAACTGATCTACATGTTCACTTCACGCTGTGTC	1586
		QY	1323	CTACCATCAGCTTACCTGGAAGAGCAGCCGCTCACCCTGAAAGCGGAGTTGGA	1382
		Db	1587	CTACCATCAGCTTACCTGGAAGAGCAGCCGCTCACCCTGAAAGCGGAGTTGGA	1643
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		Db	1644	CTCCATGCTGCTGAGGGCCACATCCTTATCTCTGCTAGGGGGATCTACCTCTCTGGG	1703
		QY	1443	CGAGTGTGGTACTTCTGCGGGCCGACGTTGTTCACTCTGGATCTCGTTATAGACAGCTA	1502
		Db	1704	CGAGTGTGGTACTTCTGCGGGCCGACGTTGTTCACTCTGGATCTCGTTATAGACAGCTA	1763
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		QY	1563	CCTGGCCATCGAGTGGTACTTCCCTCTGTTGTGTGCTGGCTGGTGTGGCTGGCTGAA	1622
		Db	1824	CCTGGCCATCGAGTGGTACTTCCCTCTGTTGTGTGCTGGCTGGTGTGGCTGGCTGAA	1883
		QY	1623	CCTGCTTTTACTATACAGTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAGAA	1682
		Db	1884	CCTGCTTTTACTATACAGTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAGAA	1943
		QY	1683	GGTCACTCTGCGGAGCTGCTGCTCTTCTGATCTACTTCTGATCTCTCTTCTGCTT	1742
		Db	1944	GGTCACTCTGCGGAGCTGCTGCTCTTCTGATCTACTTCTGATCTCTCTTCTGCTT	2003
		QY	1743	CGCTGTAGCCCTCTGTTGAGCTTCCAGGAGCTTGGCCGCCGAGAGCTCTTACAGGCC	1802
		Db	2004	CGCTGTAGCCCTCTGTTGAGCTTCCAGGAGCTTGGCCGCCGAGAGCTCTTACAGGCC	2063
		QY	1803	CAATGCCACAGAGTCAAGTCCAGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1862
		Db	2064	CAATGCCACAGAGTCAAGTCCAGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2123
		QY	1863	GTACAGGGGTATCTCTGGAAGCCCTCTCTTGGAGCTCTTCAAATTTCAACCATGGCATGGGCGA	1922

1	Renard, S. and Partiseti, M.	QY	783	GGAGAACCCACACACCGCCGCGCAGCTGCAGGCCACTGACTCCAGGGCAACACAGCTCCT	842
2	A human vanilloid receptor-like cation channel	Db	1047	GGAGAACCCACACACCGCCGCGCAGCTGCAGGCCACTGACTCCAGGGCAACACAGCTCCT	1106
3	Patent: WO 9946377-A 1 16-SEP-1999;	QY	843	GCATGCCCTAGTGATGATCTCGGACAACTCAGCTGAGAACATTGACCTGGTACACAGCAT	902
4	SANOPI SYNTHELABO (FR); RENARD STEPHANE (FR); PARTISETI MICHEL (FR)	Db	1107	GCATGCCCTAGTGATGATCTCGGACAACTCAGCTGAGAACATTGACCTGGTACACAGCAT	1166
5	Location/Qualifiers	QY	903	GTATGATGGGCTCTCCAAAGCTGGGGCCGCTCTGCTCCCTACCTGTCAGCTGAGAGCAT	962
6	1..2783	Db	1167	GTATGATGGGCTCTCCAAAGCTGGGGCCGCTCTGCTCCCTACCTGTCAGCTGAGAGCAT	1226
7	/organism="Homo sapiens"	QY	963	CGGCAACCTGCAGGATCTCAGCCCTCTGAAGCTGCGCCGCAAGGAGGGCAAGATCCAGAT	1022
8	/mol_type="unassigned DNA"	Db	1227	CGGCAACCTGCAGGATCTCAGCCCTCTGAAGCTGCGCCGCAAGGAGGGCAAGATCCAGAT	1286
9	/db_xref="taxon:9606"	QY	1023	TTTTCAGGCACATCTCTGCAGCGGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTAC	1082
10	Query Match 99.0%; Score 2444.6; DB 6; Length 2783;	Db	1287	TTTTCAGGCACATCTCTGCAGCGGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTAC	1346
11	Best Local Similarity 99.7%; Pred. No. 0;	QY	1083	CGAGTGGTGTCTATGGGCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGTGACAGCTG	1142
12	Matches 2460; Conservative 0; Mismatches 4; Indels 3; Gaps 1;	Db	1347	CGAGTGGTGTCTATGGGCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGTGACAGCTG	1406
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14		Db	1407	TCGAGAGAACTCAGTGTGGAGATCATTCGCCCTTTCATTGCAAGAGCCGACACGACCG	1466
15		QY	1203	AATGSGTCTGTTTGGAGCCCTCGAAACAACTGCTGCAGGCGAAATGGGATCTGCTCATCC	1262
16		Db	1467	AATGSGTCTGTTTGGAGCCCTCGAAACAACTGCTGCAGGCGAAATGGGATCTGCTCATCC	1526
17		QY	1263	CAAGTCTCTTAAACTCTGTGTAACTGATCTACATGTTCACTTCACGCTGTGTC	1322
18		Db	1527	CAAGTCTCTTAAACTCTGTGTAACTGATCTACATGTTCACTTCACGCTGTGTC	1586
19		QY	1323	CTACCATCAGCTTACCTGGAAGAGCAGCCGCTCACCCTGAAAGCGGAGTTGGA	1382
20		Db	1587	CTACCATCAGCTTACCTGGAAGAGCAGCCGCTCACCCTGAAAGCGGAGTTGGA	1643
21		QY	1383	CTCCATGCTGCTGAGGGCCACATCCTTATCTCTGCTAGGGGGATCTACCTCTCTGGG	1442
22		Db	1644	CTCCATGCTGCTGAGGGCCACATCCTTATCTCTGCTAGGGGGATCTACCTCTCTGGG	1703
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24		Db	1704	CGAGTGTGGTACTTCTGCGGGCCGACGTTGTTCACTCTGGATCTCGTTATAGACAGCTA	1763
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26		Db	1764	CTTTGAAATCCTCTTCTCTGTTCCAGGCCCTGCTCAGTGTGTCCAGGTGCTGTGTT	1823
27		QY	1563	CCTGGCCATCGAGTGGTACTTCCCTCTGTTGTGTGCTGGCTGGTGTGGCTGGCTGAA	1622
28		Db	1824	CCTGGCCATCGAGTGGTACTTCCCTCTGTTGTGTGCTGGCTGGTGTGGCTGGCTGAA	1883
29		QY	1623	CCTGCTTTTACTATACAGTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAGAA	1682
30		Db	1884	CCTGCTTTTACTATACAGTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAGAA	1943
31		QY	1683	GGTCACTCTGCGGAGCTGCTGCTCTTCTGATCTACTTCTGATCTCTCTTCTGCTT	1742
32		Db	1944	GGTCACTCTGCGGAGCTGCTGCTCTTCTGATCTACTTCTGATCTCTCTTCTGCTT	2003
33		QY	1743	CGCTGTAGCCCTCTGTTGAGCTTCCAGGAGCTTGGCCGCCGAGAGCTCTTACAGGCC	1802
34		Db	2004	CGCTGTAGCCCTCTGTTGAGCTTCCAGGAGCTTGGCCGCCGAGAGCTCTTACAGGCC	2063
35		QY	1803	CAATGCCACAGAGTCAAGTCCAGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1862
36		Db	2064	CAATGCCACAGAGTCAAGTCCAGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2123
37		QY	1863	GTACAGGGGTATCTCTGGAAGCCCTCTCTTGGAGCTCTTCAAATTTCAACCATGGCATGGGCGA	1922

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QY	963	CCGCAACCTCAGGATCTCAGCGCTCTGAAGCTGGCCGCCCAAGGAGGCAAGATCGAGAT	1022	
Db	1224	CCGCAACCTCAGGATCTCAGCGCTCTGAAGCTGGCCGCCCAAGGAGGCAAGATCGAGAT	1283	
QY	1023	TTTTCAGGCACATCCTCGAGCGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTTCA	1082	
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Db	1404	TGAGGAGAACTCAGTGTCTGAGATCATTTGCTTTTCAATGCAAGAGCCGCCACGACACCG	1463	
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Db	1824	CCTGGTTCATCGAGTGGTACCTGCCCTGCTTGTCTGCGCTGGTGTGCTGGGCTGGCTGAA	1883	
QY	1623	CCTGCTTTACTATACAGTGGCTTCAGACACAGGATCTACAGTGTGATGATCCAGAA	1682	
Db	1884	CCTGCTTTACTATACAGTGGCTTCCAGACACAGGATCTACAGTGTGATGATCCAGAA	1943	
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Db	1944	GGTATCCTCGGGACATGTTGGCTTCTTCTTGTGATCTTACTTACTTCTTCTTCTTCTTCTT	2003	
QY	1743	CGCTGTAGCCCTGTGTAGCCCTGAGCCAGGAGGCTTGGCGCCCGGAAAGCTCCTACAGCCC	1802	
Db	2004	CGCTGTAGCCCTGTGTAGCCCTGAGCCAGGAGGCTTGGCGCCCGGAAAGCTCCTACAGCCC	2063	
QY	1803	CAATGCCACAGAGTCAAGTGCAGCCATGGAGGGACAGGAGGACAGGGGCAACGGGGCCCA	1862	
Db	2064	CAATGCCACAGAGTCAAGTGCAGCCATGGAGGGACAGGAGGACAGGGGCAACGGGGCCCA	2123	
QY	1863	GTACAGGGGTATCTCGAAGCCTCTTGGAGCTCTTCAAAATTCACCATCGGATGGCGGA	1922	
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QY	2043	CAACAGTGTGCGCACTGACAGCTGGAGCATCTTGGAGCTGCGAAGCCATCTTGTCTCT	2102	
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Db	2364	GGAGATGGAGAAATGGCTATTGGTGTGCGAAGAGAGCGGGCGAGGTGTGATGCTGAC	2423	
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Db	2424	CGTGTGCACTAAGCCAGATGGCAGCCCGATCAGCGCTGCTTTCAGGCTGGAGAGGT	2483	
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Db	2484	GAACTGGGCTTCATGCGGAGCAGACGCTGCTACGCTGTGTGAGGACCCCTCAGGGGCGAG	2543	
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QY	2343	TGCTCTGAGGAAACTATGTGCCGTCCAGTCTCTCCAGTCCACTGATGCCACAGATG	2402	
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QY	2403	CAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCCAACCCATCTGCTGTCTGGGG	2462	
Db	2664	CAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCCAACCCATCTGCTGTCTGGGG	2723	
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QY	63	TCCTGGCTGGACGCGCAGCTTCCTCTCTAGGATGACCTCACCTCCAGCTCTCCAGT	122	

Db	324	TCCTGCTGGACCGAGCAGCCCTCTCTCTAGGATGACCTCACCCCTCCAGCTCTCCAGT	383
Qy	123	TTTCAGGTTGGAGACATTAGATGGAGCCNAGAGATGGCTCTGAGCGGACAGAGGAAA	182
Db	384	TTTCAGGTTGGAGACATTAGATGGAGCCNAGAGATGGCTCTGAGCGGACAGAGGAAA	443
Qy	183	GCTGGATTTTGGAGCGGGCTGCTCCATGGAGTCAACAGTTCCAGGGCGAGACCGGAA	242
Db	444	GCTGGATTTTGGAGCGGGCTGCTCCATGGAGTCAACAGTTCCAGGGCGAGACCGGAA	503
Qy	243	ATTGCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAAGGGAAACAGGTGCCAGTCA	302
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Db	564	GGATCCAAACCGATTGGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGCCCCGA	623
Qy	363	GGATCTGGCTGGACTTCAGAGTACCTGAGCAAGACCAGCAAGTACTCAACCGACTCGGA	422
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Qy	423	ATACACAGAGGGCTCCACAGGTAAAGCTGCTGTGATGAAGGCTGTGTGAACCTTTAAGGA	482
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Qy	663	GCATGCCCGGGCTGCGGGCGCTTCTTCCAGAGGGCCAGGAGCTTGGCTTTTATTTTCGG	722
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Qy	723	TGAGCTACCCCTCTTTTGGCGCTTGCCACCAAGCAGTGGATGTGTGAAGCTACCTTCCT	782
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Qy	783	GGAGAACCCACACACAGCCCGCCAGCTGCGAGGCCACTGACTCCAGGGCCAAACAGTCCCT	842
Db	1044	GGAGAACCCACACACAGCCCGCCAGCTGCGAGGCCACTGACTCCAGGGCCAAACAGTCCCT	1103
Qy	843	GCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAACATTTGCATGTTGGTACCAGCAT	902
Db	1104	GCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAACATTTGCATGTTGGTACCAGCAT	1163
Qy	903	GTATGATGGGCTCTCCAAAGCTGGGGCCGCTCTGCCCTACCGTGCAGCTTTGAGGACAT	962
Db	1164	GTATGATGGGCTCTCCAAAGCTGGGGCCGCTCTGCCCTACCGTGCAGCTTTGAGGACAT	1223
Qy	963	CCGCAACTGCAGGATCTCAGCCCTCTGAAGCTGGCCGCCCAAGGAGGGCAGATCGAGAT	1022
Db	1224	CCGCAACTGCAGGATCTCAGCCCTCTGAAGCTGGCCGCCCAAGGAGGGCAGATCGAGAT	1283
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Db	1284	TTTTCAGGCACTCTGACAGCGGAGTTTTCAGGACTGAGCCACTTCTTCCCGAAAGTTTCA	1343
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Qy	1143	TGAGGAGAACTCAGTGTCTGGAGATCATTTGCCCTTTTCATTTGCAAGAGCCCGCACACCG	1202
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Db	1464	AATGCTCGTTTTTGGAGCCCTTGAAACAACTGCTGAGCGGAAATGGGATCTCTCATCCC	1523
Qy	1263	CAAGTTCTTTTAAACTTCTGTGTAACTGTATCATGTTCATTTTCACTTTCACCGCTGTTCG	1322
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Qy	1323	CTACCATCAGCCTACCTTGAAAGCAGGCCGCCCTCACCTGAAAGCGGAGGTTGGAAA	1382
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Qy	1383	CTTCCATGTCTGACGGGCCACATCCTTATCTCTGTAGGGGGATCTACTCTCTCTGTGGG	1442
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Qy	1443	CGAGCTGTGTACTTCTTGGCGGGCCACGTGTTCATCTGGATCTCGTTTATGACAGCTTA	1502
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Qy	1503	CTTTGAAATCCTTCTTCCAGGCCCTGTCTCAGTGGTGTCCAGGTGTCTGTGTGT	1562
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Db	2004	CGCTGTAGCCCTTGGTGTGAGCTTGAGCCAGGAGGCTTGGCGCCCGGAAAGCTCTTACAGGCC	2063
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Db	2064	CAATGCCACAGAGTCACTGAGCCCATGGAGGACAGGAGGACAGGGCCACCGGGGCCCA	2123
Qy	1863	GTACAGGGGTATCTCGAAGCCTCTTGGAGCTCTTCAAATTCACCATCGGATGGCGGA	1922
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Qy	1923	GCTGGCTTCCAGGACAGCTGCACTTCCGCGGCATGGTGTCTGTCTGTCTGTGGCCTTA	1982
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Qy	1983	CGTGTCTCACTCACTATCTGTCTCAACATGTCTCAATTCACCATCGGATGGCGGA	2042
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 AUTHORS Young, P.E. and Ruben, S.M.  
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Db	492	ATACACAGAGGGCTCCACAGTAAAGACGTCCTGTATGTAAGCGCTGCTGTAACCTTAAGGA	551
Qy	483	CGGAGTCAATGCTCGCATCTGCACATGCTGCAGATCGACAGGACCTCTGGCAATCTCTCA	542
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Db	912	GCATGCCCTAGTGATGATCTCGACAACCTCAGCTTGAGAACTTGTCATCTGCTGACCCAGCAT	971
Qy	903	GTATGATGGGCTCTCTCAAGCTGGGGCCCGCTCTGCCCTTACCGTGCAGCTTGAGGACAT	962
Db	972	GTATGATGGGCTCTCTCAAGCTGGGGCCCGCTCTGCCCTTACCGTGCAGCTTGAGGACAT	1031
Qy	963	CCGCAACTGCAAGATCTACCGCTCTGAAGCTGGCCGCCCAAGAGGGCAAGATCGAGAT	1022
Db	1032	CCGCAACTGCAAGATCTACCGCTCTGAAGCTGGCCGCCCAAGAGGGCAAGATCGAGAT	1091
Qy	1023	TTTCAGGCACATCTGTCAGCGGGAGTTTTCAGAGACTGAGCCACCTTTCCCGAAAGTTTCAC	1082
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Qy	1143	TGAGGAAACTCAGTGTGTGAGATCATTTGCTTTTCATTTGAAGAGCCCGCACCGACACCG	1202
Db	1212	TGAGGAAACTCAGTGTGTGAGATCATTTGCTTTTCATTTGAAGAGCCCGCACCGACACCG	1271
Qy	1203	AATGGTCGTTTTGGAGCCCTGACAACTGCTGCAGCGGAATGGGATCTGTCTCATCCC	1262
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Db	1332	CAAGTCTCTTTAAACTTCTGTGTAACTCGATCTCATGTTCATCTTCAACCGCTGTTCG	1391
Qy	1323	CTACCATCAGCTTACCTGTAAGAACAGCGCCGCCCTTCACTGAAAGCGAGGTTTGGAAA	1382
Db	1392	CTACCATCAGCTTACCTGTAAGAACAGCGCCGCCCTTCACTGAAAGCGAGGTTTGGAAA	1451
Qy	1383	CTCCATGCTGTCAGCGGGCACATCTTATCTCTGCTAGGGGGATCTACCTCTCGTGGG	1442
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[illegible]

RESULT 11	
AF129112	
LOCUS	
DEFINITION	



<b>AFI29112</b>					
AFI29112.1 GI:4589140					
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
<b>REFERENCE</b>					
Caterina,M.J., Rosen,T.A., Tominaga,M., Brake,A.J. and Julius,D. A capsaicin-receptor homologue with a high threshold for noxious heat					
JOURNAL	Nature	398 (6726), 436-441 (1999)			
MEDLINE	99215558				
PUBMED	10201375				
<b>REFERENCE</b>					
AUTHORS	Caterina,M.J., Rosen,T.A., Tominaga,M., Brake,A.J. and Julius,D.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-FEB-1999) Cellular and Molecular Pharmacology, University of California, 513 Parnassus, San Francisco, CA 94143,				
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Dd	137	CGGGCTGCCTCCCATTGGAGTCAAGTTCTCAGGGCGAGACCAGAAAATTCGCCCTTCAGAT	196		
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Query Match		96.3%; Score 2378.4; DB 6; Length 2380;	
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Db	61	TTAGATGGAGGCGCAAGAGATGGCTCTGAGGCGGACAGAGGAAAGCTGGATTTTGGGAGC	120
Qy	199	GGCTGCTCCATCGAGGTCAAGTTTCAGGGCGAGGACCGGAAATTGCGCCCTCAGATA	258
Db	121	GGCTGCTCCATCGAGGTCAAGTTTCAGGGCGAGGACCGGAAATTGCGCCCTCAGATA	180
Qy	259	AGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCCAGTCAAGCGGATCCAAACCGATTT	318
Db	181	AGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCCAGTCAAGCGGATCCAAACCGATTT	240
Qy	319	GACCGAGATCGGCTCTTCAATCGCGTCTCCCGGGGTGTCCCGAGGATCTGGCTGGACTT	378
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Qy	379	CCAGGTACTCTGAGCAAGACACGCAAGTACTCTCACCGACTCGGAATACACAGAGGGTCC	438
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Qy	499	ATTCTGCCACTGCTGCAGATCGACAGGAGTCTGTGCAATCTCAGCCCTCGTAAATGTC	558
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Qy	559	CAGTGACAGATGACTATTACCGAGGCCACAGCGCTCTGCAATCGCGCAATTTGAGAAGG	618
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ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Duckworth, D.M., Davis, J.B. and Hayes, P.D.  
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